

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 19, 2005, 16:27:17 ; Search time 23 Seconds  
(without alignments)

**Title:** US-09-978-544A-523

Perfect score:

Sequence: 1 MKTIQPKMHNISWAIFTGL.....RRAGCVWLLPLLVLHLLKF 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database : Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.per.\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*

```
3: /cgn2_6/ptodata/1/1aa/6A_COMB.per:*
4: /cgn2_6/ptodata/1/1aa/6A_COMB.per:*
```

```
4: /cgn2_6/ptodata/1/1aa/6B COMB.pcp:*
```

```
3: /cgn2_6/prodata/1/iaa/PC1US COMB. pep:
6: /cgn2_6/prodata/1/iaa/backfiles1 pep:*
```

У: /cgnz v/produca/r/rad/backtires1.per:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	1806	100.0	344	4	US-09-700-397-3	Sequence 3, Appli	
2	1642	90.9	313	4	US-09-700-397-4	Sequence 4, Appli	
3	931.5	51.6	338	4	US-09-976-594-404	Sequence 404, Appl	
4	926.5	51.3	338	2	US-08-414-657D-42	Sequence 42, Appl	
5	926.5	51.3	338	2	US-08-414-657D-43	Sequence 43, Appl	
6	926.5	51.3	338	4	US-09-135-080-4	Sequence 4, Appli	
7	923.5	51.1	325	2	US-08-414-657D-2	Sequence 2, Appli	
8	923.5	51.1	325	2	US-08-414-657D-41	Sequence 41, Appli	
9	923.5	51.1	325	4	US-09-135-080-2	Sequence 2, Appli	
10	923.5	51.1	338	2	US-08-414-657D-60	Sequence 60, Appl	
11	923.5	51.1	338	4	US-09-135-080-8	Sequence 8, Appli	
12	908	50.3	308	2	US-08-414-657D-46	Sequence 46, Appl	
13	907	50.2	315	2	US-08-414-657D-47	Sequence 47, Appl	
14	905	50.1	310	2	US-08-414-657D-45	Sequence 45, Appl	
15	902	49.9	304	2	US-08-414-657D-44	Sequence 44, Appl	
16	886.5	49.1	287	2	US-08-414-657D-48	Sequence 48, Appl	
17	885.5	49.0	287	2	US-08-414-657D-49	Sequence 49, Appl	
18	796.5	44.1	252	2	US-08-414-657D-56	Sequence 56, Appl	
19	795.5	44.0	252	2	US-08-414-657D-57	Sequence 57, Appl	
20	742.5	41.1	212	4	US-09-949-016-10458	Sequence 10458, A	
21	276	15.3	588	4	US-09-949-016-10547	Sequence 10547, A	
22	267	14.8	588	4	US-09-513-999C-6852	Sequence 6852, Ap	
23	261	14.5	1395	3	US-09-540-245A-15	Sequence 15, Appl	
24	256	14.2	421	2	US-08-659-984A-1	Sequence 1, Appli	
25	256	14.2	421	3	US-08-660-531-1	Sequence 5, Appli	
26	256	14.2	444	2	US-08-659-984A-5	Sequence 5, Appli	
27	256	14.2	444	3	US-08-660-531-5	Sequence 5, Appli	

101	209	11.6	504	4	US-09-949-016-7020	Sequence 7020, Ap	174	171	9.5	1253	3	US-08-506-296B-14	Sequence 14, Appl
102	209	11.6	511	4	US-09-949-016-10054	Sequence 10054, A	175	170	9.4	318	3	US-09-068-051A-32	Sequence 32, Appl
103	208.5	11.5	1651	3	US-09-540-245A-18	Sequence 18, Appl	176	167.5	9.3	280	4	US-09-270-767-43068	Sequence 43068, A
104	205.5	11.4	596	3	US-08-752-307B-13	Sequence 13, Appl	177	167.5	9.3	466	2	US-08-432-016-4	Sequence 4, Appl
105	205.5	11.4	596	3	US-09-707-802-13	Sequence 13, Appl	178	167.5	9.3	466	2	US-08-684-594-4	Sequence 4, Appl
106	205.5	11.4	596	3	US-09-991-326-13	Sequence 13, Appl	179	167	9.2	668	1	US-08-232-538-13	Sequence 13, Appl
107	205	11.4	432	4	US-09-778-510-2	Sequence 2, Appl	180	167	9.2	668	2	US-08-786-164-13	Sequence 13, Appl
108	199	11.1	946	5	PCT-US95-08493-13	Sequence 13, Appl	181	167	9.2	764	3	US-09-142-956B-14	Sequence 14, Appl
109	191	11.0	1241	3	US-09-040-774-2	Sequence 2, Appl	182	167	9.2	767	3	US-08-874-678-2	Sequence 2, Appl
110	198	11.0	1709	4	US-09-949-016-10503	Sequence 10503, A	183	167	9.2	767	3	US-08-643-839-2	Sequence 2, Appl
111	197.5	10.9	1447	3	US-09-041-886-25	Sequence 25, Appl	184	167	9.2	767	3	US-09-348-886-2	Sequence 2, Appl
112	197.5	10.9	1447	5	PCT-US94-05277-2	Sequence 2, Appl	185	167	9.2	788	1	US-08-232-538-15	Sequence 15, Appl
113	197	10.9	1297	3	US-09-540-245A-17	Sequence 17, Appl	186	167	9.2	788	2	US-08-786-164-15	Sequence 15, Appl
114	196.5	10.9	833	4	US-09-949-016-11496	Sequence 11496, A	187	167	9.2	1356	1	US-08-810-116-8	Sequence 8, Appl
115	196.5	10.9	1180	4	US-09-949-016-6577	Sequence 6577, Ap	188	167	9.2	1356	2	US-07-930-548A-8	Sequence 8, Appl
116	195	10.8	630	2	US-08-752-307B-14	Sequence 14, Appl	189	167	9.2	1356	3	US-09-098-707A-2	Sequence 2, Appl
117	195	10.8	630	3	US-09-707-802-14	Sequence 14, Appl	190	167	9.2	1356	3	US-09-483-539-2	Sequence 2, Appl
118	195	10.8	630	3	US-09-991-326-14	Sequence 14, Appl	191	167	9.2	1356	4	US-09-949-016-6198	Sequence 6198, Ap
119	192.5	10.7	612	2	US-08-752-307B-11	Sequence 11, Appl	192	167	9.2	1456	4	US-09-949-016-9853	Sequence 9853, Ap
120	192.5	10.7	612	3	US-09-707-802-11	Sequence 11, Appl	193	166.5	9.2	302	4	US-09-877-730-14	Sequence 14, Appl
121	192.5	10.7	612	3	US-09-991-326-11	Sequence 11, Appl	194	166.5	9.2	380	4	US-09-877-730-4	Sequence 4, Appl
122	192.5	10.7	826	4	US-09-877-730-16	Sequence 16, Appl	195	166	9.2	758	2	US-08-874-678-1	Sequence 1, Appl
123	192.5	10.7	904	4	US-09-877-730-6	Sequence 6, Appl	196	166	9.2	758	3	US-08-643-839-1	Sequence 1, Appl
124	192.5	10.7	907	4	US-09-877-730-20	Sequence 20, Appl	197	166	9.2	758	3	US-09-051-363-24	Sequence 24, Appl
125	192.5	10.7	983	3	US-09-412-554A-2	Sequence 2, Appl	198	166	9.2	758	3	US-09-348-886-1	Sequence 1, Appl
126	192.5	10.7	985	4	US-09-877-730-10	Sequence 10, Appl	199	165.5	9.2	278	2	US-08-432-016-5	Sequence 5, Appl
127	192.5	10.7	991	4	US-09-877-730-12	Sequence 12, Appl	200	165.5	9.2	278	2	US-08-684-594-5	Sequence 5, Appl
128	192.5	10.7	1069	4	US-09-877-730-2	Sequence 2, Appl	201	165.5	9.2	486	2	US-08-432-016-6	Sequence 6, Appl
129	192.5	10.7	1072	4	US-09-877-730-18	Sequence 18, Appl	202	165.5	9.2	486	2	US-08-684-594-6	Sequence 6, Appl
130	192.5	10.7	1150	4	US-09-877-730-8	Sequence 8, Appl	203	165.5	9.2	583	2	US-08-432-016-2	Sequence 2, Appl
131	192.5	10.7	1260	3	US-08-506-296B-21	Sequence 21, Appl	204	165.5	9.2	583	2	US-08-684-594-2	Sequence 2, Appl
132	192.5	10.7	1268	3	US-08-506-296B-28	Sequence 28, Appl	205	165.5	9.2	646	4	US-09-949-016-6728	Sequence 6728, Ap
133	192	10.6	529	3	US-09-383-586-31	Sequence 31, Appl	206	165.5	9.2	646	4	US-09-653-961-4	Sequence 4, Appl
134	192	10.6	529	4	US-09-823-038A-31	Sequence 31, Appl	207	165.5	9.2	828	1	US-08-261-304-2	Sequence 2, Appl
135	191.5	10.6	1209	4	US-09-130-158A-2	Sequence 2, Appl	208	165.5	9.2	1617	4	US-09-784-358-16	Sequence 16, Appl
136	188.5	10.4	651	4	US-09-270-767-44877	Sequence 44877, A	209	165.5	9.2	1691	2	US-09-784-358-2	Sequence 2, Appl
137	187.5	10.4	1266	3	US-08-506-296B-4	Sequence 4, Appl	210	165	9.1	501	2	US-08-408-095-31	Sequence 31, Appl
138	185.5	10.3	318	2	US-08-633-148-4	Sequence 4, Appl	211	164	9.1	439	3	US-09-383-586-32	Sequence 32, Appl
139	185.5	10.3	332	4	US-09-062-365-1	Sequence 1, Appl	212	164	9.1	439	4	US-09-823-038A-32	Sequence 32, Appl
140	185.5	10.3	340	2	US-08-633-148-2	Sequence 2, Appl	213	164	9.1	640	4	US-09-949-016-7565	Sequence 7565, Ap
141	185.5	10.3	404	4	US-09-949-016-11025	Sequence 11025, A	214	163.5	9.1	582	4	US-09-702-705-334	Sequence 334, App
142	185.5	10.3	642	1	US-09-217-299-1	Sequence 1, Appl	215	163.5	9.1	582	4	US-09-736-457-334	Sequence 334, App
143	185.5	10.3	698	2	US-08-602-725-36	Sequence 36, Appl	216	163.5	9.1	582	4	US-09-614-124B-334	Sequence 334, App
144	185.5	10.3	702	4	US-09-949-016-6484	Sequence 6484, Ap	217	163.5	9.1	582	4	US-09-671-325-334	Sequence 334, App
145	185.5	10.3	734	2	US-08-389-459A-17	Sequence 17, Appl	218	163.5	9.1	582	4	US-09-589-184-334	Sequence 334, App
146	185.5	10.3	734	3	US-08-987-867A-17	Sequence 17, Appl	219	163.5	9.1	582	4	US-09-658-824-334	Sequence 334, App
147	185.5	10.3	740	4	US-09-949-016-8168	Sequence 8168, Ap	220	163.5	9.1	604	4	US-09-949-016-9548	Sequence 9548, Ap
148	185	10.2	1381	3	US-09-540-245A-16	Sequence 16, Appl	221	163.5	9.1	623	4	US-09-949-016-11206	Sequence 11206, A
149	184.5	10.2	66	2	US-08-414-557D-54	Sequence 54, Appl	222	163.5	9.1	646	4	US-09-653-961-2	Sequence 2, Appl
150	184.5	10.2	66	2	US-08-414-557D-55	Sequence 55, Appl	223	163.5	9.1	1745	4	US-09-800-729-89	Sequence 89, Appl
151	184.5	10.2	404	4	US-09-638-649-3	Sequence 3, Appl	224	163	9.0	924	1	US-08-481-130-28	Sequence 28, Appl
152	184.5	10.2	404	4	US-09-638-648-3	Sequence 3, Appl	225	163	9.0	924	1	US-08-656-984A-28	Sequence 28, Appl
153	184	10.2	373	4	US-09-823-038A-60	Sequence 60, Appl	226	163	9.0	924	1	US-08-485-604-28	Sequence 28, Appl
154	184	10.2	405	4	US-08-755-235-4	Sequence 4, Appl	227	163	9.0	924	2	US-08-487-595-28	Sequence 28, Appl
155	182	10.1	626	4	US-09-949-016-6213	Sequence 6213, Ap	228	162	9.0	321	6	5169835-17	Patent No. 5169835
156	182	10.1	664	4	US-09-949-016-7850	Sequence 7850, Ap	229	162	9.0	321	6	5169835-17	Patent No. 5169835
157	179	9.9	300	4	US-09-254-465A-10	Sequence 10, Appl	230	161	8.9	310	4	US-09-907-794A-423	Sequence 423, App
158	179	9.9	300	4	US-09-397-243D-12	Sequence 12, Appl	231	161	8.9	310	4	US-09-905-125A-423	Sequence 423, App
159	179	9.9	300	4	US-09-953-499-10	Sequence 10, Appl	232	161	8.9	310	4	US-09-902-775A-423	Sequence 423, App
160	174	9.6	261	4	US-09-270-767-32898	Sequence 32898, A	233	161	8.9	310	4	US-09-906-700-423	Sequence 423, App
161	174	9.6	261	4	US-09-270-767-48115	Sequence 48115, A	234	161	8.9	310	4	US-09-903-603A-423	Sequence 423, App
162	171.5	9.5	780	1	US-08-232-538-14	Sequence 14, Appl	235	161	8.9	310	4	US-09-904-920A-423	Sequence 423, App
163	171.5	9.5	780	2	US-08-786-164-14	Sequence 14, Appl	236	161	8.9	310	4	US-09-909-064-423	Sequence 423, App
164	171.5	9.5	1338	3	US-08-750-141A-3	Sequence 3, Appl	237	161	8.9	310	4	US-09-905-381A-423	Sequence 423, App
165	171.5	9.5	1338	4	US-09-119-014D-6	Sequence 6, Appl	238	161	8.9	310	4	US-09-906-618-423	Sequence 2, Appl
166	171	9.5	464	2	US-08-602-725-32	Sequence 32, Appl	239	161	8.9	622	4	US-09-499-846-2	Sequence 2, Appl
167	171	9.5	464	4	US-09-949-016-6116	Sequence 6116, Ap	240	161	8.9	806	2	US-08-443-861-5	Sequence 5, Appl
168	171	9.5	464	4	US-08-245-295-2	Sequence 2, Appl	241	161	8.9	806	3	US-08-193-829B-5	Sequence 1, Appl
169	171	9.5	917	1	US-08-481-130-2	Sequence 2, Appl	242	161	8.9	816	1	US-07-840-029-1	Sequence 1, Appl
170	171	9.5	917	1	US-08-481-130-2	Sequence 2, Appl	243	161	8.9	820	1	US-07-921-807B-3	Sequence 3, Appl
171	171	9.5	917	1	US-08-656-984A-2	Sequence 2, Appl	244	161	8.9	820	1	US-08-441-944A-3	Sequence 3, Appl
172	171	9.5	917	1	US-08-485-604-2	Sequence 2, Appl	245	161	8.9	820	3	US-08-439-992A-1	Sequence 1, Appl
173	171	9.5	917	2	US-08-487-595-2	Sequence 2, Appl	246	161	8.9	1367	2	US-08-443-861-2	Sequence 2, Appl

247	161	8.9	1367	3	US-08-193-829B-2	Sequence 2, Appli	320	155	8.6	1367	1	US-08-601-891-6	Sequence 6, Appli
248	160.5	8.9	316	4	US-09-397-243D-13	Sequence 13, Appli	321	155	8.6	1367	2	US-09-021-324-6	Sequence 6, Appli
249	160	8.9	270	4	US-09-254-465A-24	Sequence 24, Appli	322	155	8.6	1367	3	US-09-872-136B-6	Sequence 8, Appli
250	160	8.9	270	4	US-09-953-499-24	Sequence 24, Appli	323	155	8.6	1367	4	PCT-US92-02750-8	Sequence 6, Appli
251	160	8.9	273	4	US-09-254-465A-26	Sequence 26, Appli	324	155	8.6	1367	5	PCT-US92-05401-6	Sequence 6, Appli
252	160	8.9	273	4	US-09-953-499-26	Sequence 26, Appli	325	155	8.6	1367	6	PCT-US92-09893-6	Sequence 7, Appli
253	160	8.9	319	1	US-08-597-495B-22	Sequence 22, Appli	326	154.5	8.6	462	2	US-08-752-307B-7	Sequence 7, Appli
254	160	8.9	319	3	US-09-068-051A-22	Sequence 22, Appli	327	154.5	8.6	462	3	US-09-707-802-7	Sequence 7, Appli
255	160	8.9	319	4	US-09-336-536-67	Sequence 67, Appli	328	154.5	8.6	462	3	US-09-591-326-7	Sequence 7, Appli
256	160	8.9	319	4	US-09-254-465A-6	Sequence 6, Appli	329	154.5	8.6	465	2	US-08-752-307B-5	Sequence 5, Appli
257	160	8.9	319	4	US-09-953-499-6	Sequence 6, Appli	330	154.5	8.6	465	2	US-09-707-802-5	Sequence 5, Appli
258	160	8.9	609	4	US-09-949-016-7747	Sequence 7747, Ap	331	154.5	8.6	465	3	US-09-991-326-5	Sequence 5, Appli
259	160	8.9	609	4	US-09-949-016-7748	Sequence 7748, Ap	332	154.5	8.6	602	1	US-08-428-926-5	Sequence 5, Appli
260	160	8.9	609	4	US-09-949-016-7749	Sequence 7749, Ap	333	154.5	8.6	602	1	US-08-428-927-5	Sequence 5, Appli
261	160	8.9	609	4	US-09-949-016-7750	Sequence 7750, Ap	334	154.5	8.6	602	1	US-08-428-298-5	Sequence 5, Appli
262	160	8.9	609	4	US-09-949-016-7751	Sequence 7751, Ap	335	154.5	8.6	602	1	US-08-339-517-5	Sequence 5, Appli
263	160	8.9	609	4	US-09-949-016-7752	Sequence 7752, Ap	336	154.5	8.6	1311	3	US-08-340-011-5	Sequence 5, Appli
264	160	8.9	609	4	US-09-949-016-7753	Sequence 7753, Ap	337	154.5	8.6	1311	3	US-08-901-710-5	Sequence 5, Appli
265	160	8.9	609	4	US-09-949-016-7754	Sequence 7754, Ap	338	154.5	8.6	1311	4	US-09-169-079-5	Sequence 5, Appli
266	160	8.9	817	1	US-07-640-029-2	Sequence 2, Appli	339	154	8.5	579	3	US-09-173-151A-2	Sequence 2, Appli
267	160	8.9	822	1	US-07-921-807B-4	Sequence 4, Appli	340	154	8.5	579	3	US-09-173-151A-4	Sequence 2, Appli
268	160	8.9	822	1	US-08-459-296-2	Sequence 2, Appli	341	153.5	8.5	477	2	US-08-432-016-3	Sequence 3, Appli
269	160	8.9	822	1	US-08-441-944A-4	Sequence 4, Appli	342	153.5	8.5	477	2	US-08-684-594-3	Sequence 3, Appli
270	160	8.9	822	2	US-08-451-822A-12	Sequence 12, Appli	343	153	8.5	189	4	US-09-270-767-32726	Sequence 32726, A
271	160	8.9	822	3	US-08-439-992A-2	Sequence 2, Appli	344	153	8.5	189	4	US-09-270-767-47943	Sequence 47943, A
272	160	8.9	822	3	US-08-323-430-12	Sequence 12, Appli	345	153	8.5	524	4	US-09-270-767-44009	Sequence 44009, A
273	159	8.8	822	1	US-07-997-133-1	Sequence 1, Appli	346	153	8.5	894	4	US-09-949-016-10605	Sequence 10605, A
274	158.5	8.8	1474	4	US-09-677-046A-4	Sequence 4, Appli	347	152	8.4	351	5	PCT-US93-05703-2	Sequence 2, Appli
275	158.5	8.8	1509	4	US-09-677-046A-2	Sequence 2, Appli	348	152	8.4	1123	4	US-09-949-016-6230	Sequence 6230, Ap
276	158	8.7	292	4	US-09-800-729-175	Sequence 175, App	349	152	8.4	1123	4	US-09-949-016-7532	Sequence 7532, Ap
277	158	8.7	611	2	US-08-752-307B-10	Sequence 10, Appli	350	151.5	8.4	227	4	US-09-205-258-947	Sequence 947, App
278	158	8.7	611	3	US-09-707-802-10	Sequence 10, Appli	351	151.5	8.4	365	4	US-09-949-016-7591	Sequence 7591, Ap
279	158	8.7	611	3	US-09-991-326-10	Sequence 10, Appli	352	151.5	8.4	422	1	US-08-036-555B-170	Sequence 170, App
280	158	8.7	736	5	PCT-US93-00031-15	Sequence 15, Appli	353	151.5	8.4	422	1	US-08-469-569-170	Sequence 170, App
281	157.5	8.7	1503	4	US-09-677-046A-6	Sequence 6, Appli	354	151.5	8.4	422	1	US-08-428-926-3	Sequence 3, Appli
282	157	8.7	260	4	US-09-254-465A-23	Sequence 23, Appli	355	151.5	8.4	422	1	US-08-249-322A-170	Sequence 3, Appli
283	157	8.7	260	4	US-09-953-499-23	Sequence 23, Appli	356	151.5	8.4	422	1	US-08-428-927-3	Sequence 3, Appli
284	157	8.7	263	4	US-09-254-465A-25	Sequence 25, Appli	357	151.5	8.4	422	1	US-08-428-298-3	Sequence 3, Appli
285	157	8.7	263	4	US-09-953-499-25	Sequence 25, Appli	358	151.5	8.4	422	1	US-08-339-517-3	Sequence 3, Appli
286	157	8.7	293	3	US-09-188-930-331	Sequence 331, App	359	151.5	8.4	422	1	US-08-469-526A-170	Sequence 170, App
287	157	8.7	293	3	US-09-462-270-2	Sequence 2, Appli	360	151.5	8.4	422	2	US-08-734-591A-170	Sequence 170, App
288	157	8.7	293	4	US-09-254-465A-1	Sequence 1, Appli	361	151.5	8.4	422	2	US-08-469-660-170	Sequence 170, App
289	157	8.7	299	4	US-09-312-283C-189	Sequence 189, App	362	151.5	8.4	422	3	US-08-341-018-72	Sequence 72, Appli
290	157	8.7	299	4	US-09-312-283C-331	Sequence 331, App	363	151.5	8.4	422	3	US-08-470-335-170	Sequence 170, App
291	157	8.7	299	4	US-09-907-794A-119	Sequence 119, App	364	151.5	8.4	422	3	US-08-735-021-170	Sequence 170, App
292	157	8.7	299	4	US-09-905-125A-119	Sequence 119, App	365	151.5	8.4	422	3	US-08-734-664A-170	Sequence 170, App
293	157	8.7	299	4	US-09-902-775A-119	Sequence 119, App	366	151.5	8.4	422	3	US-08-470-339-170	Sequence 170, App
294	157	8.7	299	4	US-09-397-243D-3	Sequence 3, Appli	367	151.5	8.4	422	4	US-08-467-602-170	Sequence 170, App
295	157	8.7	299	4	US-09-906-700-119	Sequence 119, App	368	151.5	8.4	422	4	US-08-411-295F-65	Sequence 65, Appli
296	157	8.7	299	4	US-09-903-603A-119	Sequence 119, App	369	151.5	8.4	422	4	US-08-411-295F-66	Sequence 66, Appli
297	157	8.7	299	4	US-09-904-920A-119	Sequence 119, App	370	151.5	8.4	422	4	US-08-411-295F-69	Sequence 69, Appli
298	157	8.7	299	4	US-09-909-064-119	Sequence 119, App	371	151.5	8.4	422	4	US-08-411-295F-103	Sequence 103, App
299	157	8.7	299	4	US-09-905-381A-119	Sequence 119, App	372	151.5	8.4	422	5	PCT-US94-05083C-166	Sequence 166, App
300	157	8.7	299	4	US-09-906-618-119	Sequence 119, App	373	151.5	8.4	422	5	PCT-US94-05083C-185	Sequence 185, App
301	157	8.7	299	4	US-09-953-499-1	Sequence 1, Appli	374	151.5	8.4	422	5	PCT-US95-06846A-170	Sequence 170, App
302	156.5	8.7	416	4	US-09-638-649-1	Sequence 1, Appli	375	151.5	8.4	1363	2	US-08-874-678-32	Sequence 32, Appli
303	156.5	8.7	416	4	US-08-755-235-2	Sequence 2, Appli	376	151.5	8.4	1363	3	US-08-643-839-32	Sequence 32, Appli
304	156.5	8.7	416	4	US-09-638-648-1	Sequence 1, Appli	377	151.5	8.4	1363	3	US-09-348-886-32	Sequence 32, Appli
305	155.5	8.6	299	3	US-09-188-930-189	Sequence 189, App	378	151	8.4	874	2	US-08-456-647B-6	Sequence 6, Appli
306	155.5	8.6	880	1	US-08-445-640-10	Sequence 10, Appli	379	151	8.4	874	2	US-08-237-401A-6	Sequence 4, Appli
307	155.5	8.6	880	3	US-08-170-558-10	Sequence 10, Appli	380	150.5	8.3	349	4	US-09-924-103-4	Sequence 189, App
308	155.5	8.6	880	3	US-08-447-314-10	Sequence 10, Appli	381	150.5	8.3	411	3	US-08-470-339-188	Sequence 188, App
309	155.5	8.6	880	3	US-08-445-461-10	Sequence 10, Appli	382	150.5	8.3	411	3	US-08-470-339-188	Sequence 188, App
310	155.5	8.6	880	4	US-09-223-490-10	Sequence 10, Appli	383	150.5	8.3	422	4	US-08-467-602-324	Sequence 324, App
311	155	8.6	805	3	US-08-985-526-34	Sequence 34, Appli	384	150.5	8.3	422	4	US-08-411-295F-250	Sequence 250, App
312	155	8.6	1248	4	US-09-949-016-10595	Sequence 10595, A	385	150.5	8.3	425	3	US-08-470-335-226	Sequence 226, App
313	155	8.6	1248	4	US-09-949-016-10596	Sequence 10596, A	386	150.5	8.3	425	4	US-08-467-602-320	Sequence 320, App
314	155	8.6	1363	4	US-09-375-248-19	Sequence 19, Appli	387	150.5	8.3	425	4	US-08-411-295F-246	Sequence 246, App
315	155	8.6	1367	1	US-07-813-593-4	Sequence 4, Appli	388	150.5	8.3	445	4	US-08-467-602-338	Sequence 328, App
316	155	8.6	1367	1	US-07-977-451-6	Sequence 6, Appli	389	150.5	8.3	445	4	US-08-411-295F-254	Sequence 254, App
317	155	8.6	1367	1	US-07-946-507-4	Sequence 4, Appli	390	150.5	8.3	456	4	US-08-467-602-366	Sequence 366, App
318	155	8.6	1367	1	US-08-252-517-6	Sequence 6, Appli	391	150.5	8.3	456	4	US-08-411-295F-292	Sequence 292, App
319	155	8.6	1367	1	US-07-906-397A-6	Sequence 6, Appli	392	150.5	8.3	459	4	US-08-467-602-362	Sequence 362, App

393	150.5	8.3	459	4	US-08-411-295F-288	Sequence 288, App	466	150.5	8.3	884	4	US-08-411-295F-304	Sequence 304, App
394	150.5	8.3	479	4	US-08-467-602-370	Sequence 370, App	467	150.5	8.3	888	4	US-08-467-602-325	Sequence 325, App
395	150.5	8.3	479	4	US-08-411-295F-296	Sequence 296, App	468	150.5	8.3	888	4	US-08-411-295F-251	Sequence 251, App
396	150.5	8.3	601	3	US-08-470-335-233	Sequence 233, App	469	150.5	8.3	897	4	US-08-467-602-337	Sequence 337, App
397	150.5	8.3	601	4	US-08-467-602-323	Sequence 323, App	470	150.5	8.3	897	4	US-08-411-295F-263	Sequence 263, App
398	150.5	8.3	601	4	US-08-411-295F-227	Sequence 227, App	471	150.5	8.3	899	4	US-08-467-602-364	Sequence 364, App
399	150.5	8.3	604	3	US-08-470-335-227	Sequence 227, App	472	150.5	8.3	899	4	US-08-411-295F-290	Sequence 290, App
400	150.5	8.3	604	4	US-08-467-602-318	Sequence 318, App	473	150.5	8.3	902	4	US-08-467-602-359	Sequence 359, App
401	150.5	8.3	604	4	US-08-411-295F-244	Sequence 244, App	474	150.5	8.3	902	4	US-08-411-295F-285	Sequence 285, App
402	150.5	8.3	610	3	US-08-470-335-236	Sequence 236, App	475	150.5	8.3	908	4	US-08-467-602-376	Sequence 376, App
403	150.5	8.3	610	4	US-08-467-602-332	Sequence 332, App	476	150.5	8.3	908	4	US-08-411-295F-302	Sequence 302, App
404	150.5	8.3	610	4	US-08-411-295F-258	Sequence 258, App	477	150.5	8.3	911	4	US-08-467-602-373	Sequence 373, App
405	150.5	8.3	613	3	US-08-470-335-230	Sequence 230, App	478	150.5	8.3	911	4	US-08-411-295F-299	Sequence 299, App
406	150.5	8.3	613	4	US-08-467-602-329	Sequence 329, App	479	150.5	8.3	922	4	US-08-467-602-367	Sequence 367, App
407	150.5	8.3	613	4	US-08-411-295F-255	Sequence 255, App	480	150.5	8.3	922	4	US-08-411-295F-293	Sequence 293, App
408	150.5	8.3	624	4	US-08-467-602-360	Sequence 360, App	481	150.5	8.3	931	4	US-08-467-602-379	Sequence 379, App
409	150.5	8.3	624	4	US-08-411-295F-252	Sequence 252, App	482	150.5	8.3	931	4	US-08-411-295F-305	Sequence 305, App
410	150.5	8.3	633	4	US-08-467-602-335	Sequence 335, App	483	150.5	8.3	1298	1	US-08-222-616-33	Sequence 33, Appli
411	150.5	8.3	633	4	US-08-411-295F-261	Sequence 261, App	484	150.5	8.3	1298	1	US-08-340-011-2	Sequence 2, Appli
412	150.5	8.3	635	4	US-08-467-602-365	Sequence 365, App	485	150.5	8.3	1298	3	US-08-901-710-2	Sequence 2, Appli
413	150.5	8.3	635	4	US-08-411-295F-291	Sequence 291, App	486	150.5	8.3	1298	3	US-08-446-648-33	Sequence 33, Appli
414	150.5	8.3	638	4	US-08-467-602-360	Sequence 360, App	487	150.5	8.3	1298	4	US-09-982-610-33	Sequence 33, Appli
415	150.5	8.3	638	4	US-08-411-295F-286	Sequence 286, App	488	150.5	8.3	1298	4	US-09-169-079-2	Sequence 2, Appli
416	150.5	8.3	644	4	US-08-467-602-374	Sequence 374, App	489	150.5	8.3	1298	5	PCT-US95-04228-33	Sequence 33, Appli
417	150.5	8.3	644	4	US-08-411-295F-300	Sequence 300, App	490	150.5	8.3	1362	2	US-08-874-678-33	Sequence 33, Appli
418	150.5	8.3	647	4	US-08-467-602-371	Sequence 371, App	491	150.5	8.3	1362	3	US-08-643-839-33	Sequence 33, Appli
419	150.5	8.3	647	4	US-08-411-295F-297	Sequence 297, App	492	150.5	8.3	1362	3	US-09-348-886-33	Sequence 33, Appli
420	150.5	8.3	658	4	US-08-467-602-368	Sequence 368, App	493	150.5	8.3	1363	1	US-08-340-011-4	Sequence 4, Appli
421	150.5	8.3	658	4	US-08-411-295F-294	Sequence 294, App	494	150.5	8.3	1363	3	US-08-901-710-4	Sequence 4, Appli
422	150.5	8.3	667	4	US-08-467-602-377	Sequence 377, App	495	150.5	8.3	1363	4	US-09-375-248-2	Sequence 2, Appli
423	150.5	8.3	667	4	US-08-411-295F-303	Sequence 303, App	496	150.5	8.3	1363	4	US-09-169-079-4	Sequence 4, Appli
424	150.5	8.3	777	2	US-08-874-678-3	Sequence 3, Appli	497	150.5	8.3	1368	2	US-08-874-678-34	Sequence 34, Appli
425	150.5	8.3	777	3	US-08-643-839-3	Sequence 3, Appli	498	150.5	8.3	1368	3	US-08-643-839-34	Sequence 34, Appli
426	150.5	8.3	777	3	US-09-348-886-3	Sequence 3, Appli	499	150.5	8.3	1368	3	US-09-348-886-34	Sequence 34, Appli
427	150.5	8.3	818	3	US-08-470-335-234	Sequence 234, App	500	150	8.3	355	1	US-08-471-570-14	Sequence 14, Appli
428	150.5	8.3	818	4	US-08-467-602-321	Sequence 321, App	501	150	8.3	643	1	US-08-471-570-6	Sequence 6, Appli
429	150.5	8.3	818	4	US-08-411-295F-247	Sequence 247, App	502	150	8.3	769	1	US-08-471-570-8	Sequence 8, Appli
430	150.5	8.3	821	3	US-08-470-335-228	Sequence 228, App	503	149.5	8.3	1501	2	US-08-447-464-3	Sequence 3, Appli
431	150.5	8.3	821	4	US-08-467-602-319	Sequence 319, App	504	149.5	8.3	1501	2	US-08-716-679-3	Sequence 3, Appli
432	150.5	8.3	821	4	US-08-411-295F-245	Sequence 245, App	505	149	8.3	388	1	US-08-429-742-4	Sequence 4, Appli
433	150.5	8.3	827	3	US-08-470-335-237	Sequence 237, App	506	148.5	8.2	1911	1	US-08-348-006B-5	Sequence 5, Appli
434	150.5	8.3	827	4	US-08-467-602-333	Sequence 333, App	507	148.5	8.2	1911	2	US-08-800-825A-5	Sequence 5, Appli
435	150.5	8.3	827	4	US-08-411-295F-259	Sequence 259, App	508	148.5	8.2	1911	3	US-09-158-657-5	Sequence 5, Appli
436	150.5	8.3	830	3	US-08-470-335-231	Sequence 231, App	509	148.5	8.2	1911	5	PCT-US94-10166-5	Sequence 5, Appli
437	150.5	8.3	830	4	US-08-467-602-330	Sequence 330, App	510	148	8.2	602	1	US-08-168-092A-2	Sequence 2, Appli
438	150.5	8.3	830	4	US-08-411-295F-256	Sequence 256, App	511	148	8.2	820	1	US-08-166-717D-6	Sequence 6, Appli
439	150.5	8.3	841	4	US-08-467-602-327	Sequence 327, App	512	147.5	8.2	403	4	US-09-638-649-5	Sequence 5, Appli
440	150.5	8.3	841	4	US-08-411-295F-253	Sequence 253, App	513	147.5	8.2	403	4	US-09-638-648-5	Sequence 5, Appli
441	150.5	8.3	850	4	US-08-467-602-336	Sequence 336, App	514	145.5	8.1	252	4	US-09-270-767-4627	Sequence 4627, A
442	150.5	8.3	850	4	US-08-411-295F-262	Sequence 262, App	515	145.5	8.1	549	4	US-09-858-664A-5	Sequence 5, Appli
443	150.5	8.3	852	4	US-08-467-602-363	Sequence 363, App	516	145.5	8.1	549	4	US-10-274-978-6	Sequence 6, Appli
444	150.5	8.3	852	4	US-08-411-295F-289	Sequence 289, App	517	145.5	8.1	549	4	US-10-697-263-6	Sequence 6, Appli
445	150.5	8.3	855	4	US-08-467-602-361	Sequence 361, App	518	145	8.0	972	3	US-08-750-141A-2	Sequence 10, Appli
446	150.5	8.3	855	4	US-08-411-295F-287	Sequence 287, App	519	145	8.0	972	4	US-09-944-807-10	Sequence 10, Appli
447	150.5	8.3	861	4	US-08-467-602-375	Sequence 375, App	520	144	8.0	891	4	US-09-145-473B-25	Sequence 25, Appli
448	150.5	8.3	861	4	US-08-411-295F-301	Sequence 301, App	521	143.5	7.9	344	2	US-08-602-725-34	Sequence 34, Appli
449	150.5	8.3	864	4	US-08-467-602-372	Sequence 372, App	522	143.5	7.9	662	1	US-08-261-304-7	Sequence 7, Appli
450	150.5	8.3	864	4	US-08-411-295F-298	Sequence 298, App	523	143	7.9	661	2	US-08-232-538-12	Sequence 12, Appli
451	150.5	8.3	865	3	US-08-470-335-235	Sequence 235, App	524	143	7.9	661	2	US-08-786-164-12	Sequence 12, Appli
452	150.5	8.3	865	4	US-08-467-602-322	Sequence 322, App	525	143	7.9	687	1	US-08-232-538-6	Sequence 6, Appli
453	150.5	8.3	865	4	US-08-411-295F-248	Sequence 248, App	526	143	7.9	687	2	US-08-786-164-6	Sequence 6, Appli
454	150.5	8.3	868	3	US-08-470-335-229	Sequence 229, App	527	143	7.9	687	3	US-09-427-353-2	Sequence 2, Appli
455	150.5	8.3	868	4	US-08-467-602-317	Sequence 317, App	528	142.5	7.9	263	4	US-08-411-295F-77	Sequence 77, Appli
456	150.5	8.3	868	4	US-08-411-295F-243	Sequence 243, App	529	142.5	7.9	431	4	US-09-592-998C-9	Sequence 9, Appli
457	150.5	8.3	874	3	US-08-470-335-238	Sequence 238, App	530	142.5	7.9	435	4	US-09-592-998C-10	Sequence 10, Appli
458	150.5	8.3	874	4	US-08-467-602-334	Sequence 334, App	531	142.5	7.9	735	5	PCT-US93-00031-13	Sequence 13, Appli
459	150.5	8.3	874	4	US-08-411-295F-260	Sequence 260, App	532	142.5	7.9	739	3	US-08-482-073-6	Sequence 6, Appli
460	150.5	8.3	875	4	US-08-467-602-369	Sequence 369, App	533	142.5	7.9	739	5	PCT-US93-00031-9	Sequence 9, Appli
461	150.5	8.3	875	4	US-08-411-295F-295	Sequence 295, App	534	141.5	7.8	234	3	US-08-470-335-193	Sequence 193, App
462	150.5	8.3	877	3	US-08-470-335-232	Sequence 232, App	535	141.5	7.8	257	3	US-08-341-018-6	Sequence 6, Appli
463	150.5	8.3	877	4	US-08-467-602-331	Sequence 331, App	536	141.5	7.8	257	3	US-08-470-339-193	Sequence 193, App
464	150.5	8.3	877	4	US-08-411-295F-257	Sequence 257, App	537	141.5	7.8	257	4	US-08-467-602-387	Sequence 387, App
465	150.5	8.3	884	4	US-08-467-602-378	Sequence 378, App	538	141.5	7.8	257	4	US-08-411-295F-6	Sequence 6, Appli



539	141.5	7.8	263	4	US-08-411-295F-4	Sequence 4, Appli	612	139.5	7.7	263	3	US-08-341-018-4	Sequence 4, Appli
540	141.5	7.8	280	3	US-08-341-018-56	Sequence 56, Appl	613	139.5	7.7	263	3	US-08-470-335-191	Sequence 191, App
541	141.5	7.8	280	3	US-08-470-335-192	Sequence 192, App	614	139.5	7.7	263	3	US-08-470-339-191	Sequence 191, App
542	141.5	7.8	280	3	US-08-470-339-192	Sequence 192, App	615	139.5	7.7	263	3	US-08-467-602-385	Sequence 385, App
543	141.5	7.8	280	4	US-08-467-602-386	Sequence 386, App	616	139.5	7.7	419	6	5169835-2	Patent No. 5169835
544	141.5	7.8	280	4	US-08-411-295F-49	Sequence 49, Appl	617	139.5	7.7	419	6	5169835-2	Patent No. 5169835
545	141.5	7.8	280	4	US-08-411-295F-95	Sequence 95, Appl	618	139	7.7	272	1	US-08-282-951-6	Sequence 6, Appli
546	141.5	7.8	388	1	US-08-445-640-12	Sequence 12, Appl	619	138.5	7.7	140	3	US-08-986-485-4	Sequence 4, Appli
547	141.5	7.8	388	3	US-08-170-558-12	Sequence 12, Appl	620	138.5	7.7	173	4	US-08-467-602-240	Sequence 240, App
548	141.5	7.8	388	3	US-08-447-314-12	Sequence 12, Appl	621	138.5	7.7	173	4	US-08-411-295F-166	Sequence 166, App
549	141.5	7.8	388	3	US-08-445-641-12	Sequence 12, Appl	622	138.5	7.7	176	4	US-08-467-602-236	Sequence 236, App
550	141.5	7.8	388	4	US-09-223-490-12	Sequence 12, Appl	623	138.5	7.7	176	4	US-08-411-295F-162	Sequence 162, App
551	141	7.8	471	4	US-09-949-016-9042	Sequence 9042, Ap	624	138.5	7.7	196	4	US-08-467-602-244	Sequence 244, App
552	141	7.8	471	4	US-09-949-016-9043	Sequence 9043, Ap	625	138.5	7.7	196	4	US-08-411-295F-170	Sequence 170, App
553	141	7.8	471	4	US-09-949-016-9044	Sequence 9044, Ap	626	138.5	7.7	207	4	US-08-467-602-282	Sequence 282, App
554	141	7.8	471	4	US-09-949-016-9045	Sequence 9045, Ap	627	138.5	7.7	207	4	US-08-411-295F-208	Sequence 208, App
555	141	7.8	471	4	US-09-949-016-9046	Sequence 9046, Ap	628	138.5	7.7	210	4	US-08-467-602-278	Sequence 278, App
556	141	7.8	471	4	US-09-949-016-9047	Sequence 9047, Ap	629	138.5	7.7	210	4	US-08-411-295F-204	Sequence 204, App
557	141	7.8	471	4	US-09-949-016-9048	Sequence 9048, Ap	630	138.5	7.7	230	4	US-08-467-602-286	Sequence 286, App
558	141	7.8	471	4	US-09-949-016-9049	Sequence 9049, Ap	631	138.5	7.7	230	4	US-08-411-295F-212	Sequence 212, App
559	141	7.8	471	4	US-09-949-016-9050	Sequence 9050, Ap	632	138.5	7.7	352	4	US-08-467-602-239	Sequence 239, App
560	141	7.8	471	4	US-09-949-016-9051	Sequence 9051, Ap	633	138.5	7.7	352	4	US-08-411-295F-165	Sequence 165, App
561	141	7.8	821	2	US-08-451-822A-13	Sequence 13, Appl	634	138.5	7.7	355	4	US-08-467-602-234	Sequence 234, App
562	141	7.8	821	3	US-08-323-430-13	Sequence 13, Appl	635	138.5	7.7	355	4	US-08-411-295F-160	Sequence 160, App
563	140.5	7.8	257	4	US-08-411-295F-78	Sequence 78, Appl	636	138.5	7.7	361	4	US-08-467-602-248	Sequence 248, App
564	140.5	7.8	552	4	US-09-969-532-8	Sequence 8, Appli	637	138.5	7.7	361	4	US-08-411-295F-174	Sequence 174, App
565	140.5	7.8	563	4	US-09-969-532-6	Sequence 6, Appli	638	138.5	7.7	364	4	US-08-467-602-245	Sequence 245, App
566	140.5	7.8	566	4	US-09-969-532-4	Sequence 4, Appli	639	138.5	7.7	364	4	US-08-411-295F-171	Sequence 171, App
567	140.5	7.8	577	4	US-09-969-532-12	Sequence 12, Appli	640	138.5	7.7	375	4	US-08-467-602-242	Sequence 242, App
568	140.5	7.8	589	4	US-09-866-510-12	Sequence 12, Appl	641	138.5	7.7	375	4	US-08-411-295F-168	Sequence 168, App
569	140.5	7.8	762	4	US-09-949-016-7568	Sequence 7568, Ap	642	138.5	7.7	384	4	US-08-467-602-251	Sequence 251, App
570	140.5	7.8	886	4	US-09-969-532-16	Sequence 16, Appl	643	138.5	7.7	384	4	US-08-411-295F-177	Sequence 177, App
571	140.5	7.8	897	4	US-09-969-532-14	Sequence 14, Appl	644	138.5	7.7	386	4	US-08-467-602-281	Sequence 281, App
572	140.5	7.8	900	4	US-09-969-532-12	Sequence 12, Appl	645	138.5	7.7	386	4	US-08-411-295F-207	Sequence 207, App
573	140.5	7.8	911	4	US-09-969-532-10	Sequence 10, Appl	646	138.5	7.7	389	4	US-08-467-602-276	Sequence 276, App
574	140.5	7.8	1088	4	US-09-961-403-4	Sequence 4, Appli	647	138.5	7.7	389	4	US-08-411-295F-202	Sequence 202, App
575	140.5	7.8	1089	1	US-08-180-195-36	Sequence 36, Appl	648	138.5	7.7	395	4	US-08-467-602-290	Sequence 290, App
576	140.5	7.8	1089	1	US-08-168-917-4	Sequence 4, Appli	649	138.5	7.7	395	4	US-08-411-295F-216	Sequence 216, App
577	140.5	7.8	1089	1	US-08-477-329-36	Sequence 36, Appl	650	138.5	7.7	398	4	US-08-467-602-287	Sequence 287, App
578	140.5	7.8	1089	2	US-08-475-458-36	Sequence 36, Appl	651	138.5	7.7	398	4	US-08-411-295F-213	Sequence 213, App
579	140.5	7.8	1089	2	US-08-460-510-4	Sequence 4, Appli	652	138.5	7.7	409	4	US-08-467-602-284	Sequence 284, App
580	140.5	7.8	1089	2	US-08-460-490-4	Sequence 4, Appli	653	138.5	7.7	409	4	US-08-411-295F-210	Sequence 210, App
581	140.5	7.8	1089	3	US-08-980-400-36	Sequence 36, Appl	654	138.5	7.7	418	4	US-08-467-602-293	Sequence 293, App
582	140.5	7.8	1089	3	US-08-462-728-2	Sequence 2, Appli	655	138.5	7.7	418	4	US-08-411-295F-219	Sequence 219, App
583	140.5	7.8	1089	3	US-09-583-459A-36	Sequence 36, Appl	656	138.5	7.7	569	4	US-08-467-602-237	Sequence 237, App
584	140.5	7.8	1089	3	US-09-583-210-36	Sequence 36, Appl	657	138.5	7.7	569	4	US-08-411-295F-163	Sequence 163, App
585	140.5	7.8	1089	3	US-09-583-449A-36	Sequence 36, Appl	658	138.5	7.7	572	4	US-08-467-602-235	Sequence 235, App
586	140.5	7.8	1089	3	US-09-435-059-36	Sequence 36, Appl	659	138.5	7.7	572	4	US-08-411-295F-161	Sequence 161, App
587	140.5	7.8	1089	3	US-08-461-917-2	Sequence 2, Appli	660	138.5	7.7	578	4	US-08-467-602-249	Sequence 249, App
588	140.5	7.8	1089	4	US-08-464-436-2	Sequence 2, Appli	661	138.5	7.7	578	4	US-08-411-295F-175	Sequence 175, App
589	140.5	7.8	1089	4	US-08-454-436-2	Sequence 2, Appli	662	138.5	7.7	581	4	US-08-467-602-246	Sequence 246, App
590	140.5	7.8	1089	4	US-09-769-387-2	Sequence 2, Appli	663	138.5	7.7	581	4	US-08-411-295F-172	Sequence 172, App
591	140.5	7.8	1089	4	US-09-866-510-2	Sequence 2, Appli	664	138.5	7.7	592	4	US-08-467-602-243	Sequence 243, App
592	140.5	7.8	1089	4	US-09-866-510-4	Sequence 4, Appli	665	138.5	7.7	592	4	US-08-411-295F-169	Sequence 169, App
593	140.5	7.8	1089	4	US-09-866-510-6	Sequence 6, Appli	666	138.5	7.7	601	4	US-08-467-602-252	Sequence 252, App
594	140.5	7.8	1089	4	US-09-866-510-8	Sequence 8, Appli	667	138.5	7.7	601	4	US-08-411-295F-178	Sequence 178, App
595	140.5	7.8	1089	4	US-09-866-510-10	Sequence 10, Appl	668	138.5	7.7	603	4	US-08-467-602-279	Sequence 279, App
596	140.5	7.8	1089	4	US-09-919-497-90	Sequence 90, Appl	669	138.5	7.7	603	4	US-08-411-295F-205	Sequence 205, App
597	140.5	7.8	1089	4	US-09-949-016-6703	Sequence 6703, Ap	670	138.5	7.7	606	4	US-08-467-602-277	Sequence 277, App
598	140.5	7.8	1089	5	PCT-US92-00730-4	Sequence 4, Appli	671	138.5	7.7	606	4	US-08-411-295F-203	Sequence 203, App
599	140.5	7.8	1089	5	PCT-US92-00862-4	Sequence 4, Appli	672	138.5	7.7	612	4	US-08-467-602-291	Sequence 291, App
600	140	7.8	203	4	US-09-270-767-60345	Sequence 60345, A	673	138.5	7.7	612	4	US-08-411-295F-217	Sequence 217, App
601	140	7.8	801	3	US-09-383-630-6	Sequence 6, Appli	674	138.5	7.7	615	4	US-08-467-602-288	Sequence 288, App
602	140	7.8	890	1	US-08-445-640-2	Sequence 2, Appli	675	138.5	7.7	615	4	US-08-411-295F-214	Sequence 214, App
603	140	7.8	890	3	US-08-170-558-2	Sequence 2, Appli	676	138.5	7.7	616	4	US-08-467-602-238	Sequence 238, App
604	140	7.8	890	3	US-08-447-314-2	Sequence 2, Appli	677	138.5	7.7	616	4	US-08-411-295F-164	Sequence 164, App
605	140	7.8	890	3	US-08-445-461-2	Sequence 2, Appli	678	138.5	7.7	619	4	US-08-467-602-233	Sequence 233, App
606	140	7.8	890	4	US-09-223-490-2	Sequence 2, Appli	679	138.5	7.7	619	4	US-08-411-295F-159	Sequence 159, App
607	140	7.8	911	1	US-08-286-305A-1	Sequence 1, Appli	680	138.5	7.7	625	4	US-08-467-602-250	Sequence 250, App
608	140	7.8	911	2	US-08-441-104A-1	Sequence 1, Appli	681	138.5	7.7	625	4	US-08-411-295F-176	Sequence 176, App
609	140	7.8	911	2	US-08-440-816A-1	Sequence 1, Appli	682	138.5	7.7	626	4	US-08-467-602-285	Sequence 285, App
610	140	7.8	911	3	US-09-417-381A-1	Sequence 1, Appli	683	138.5	7.7	626	4	US-08-411-295F-211	Sequence 211, App
611	140	7.8	976	3	US-08-750-141A-1	Sequence 1, Appli	684	138.5	7.7	628	4	US-08-467-602-247	Sequence 247, App

685	138.5	7.7	628	4	US-08-411-295F-173	Sequence 173, App	758	134.5	7.4	644	3	US-08-470-335-250	Sequence 250, App
686	138.5	7.7	635	4	US-08-467-602-294	Sequence 294, App	759	134.5	7.4	644	4	US-08-467-602-311	Sequence 311, App
687	138.5	7.7	635	4	US-08-411-295F-220	Sequence 220, App	760	134.5	7.4	644	4	US-08-411-295F-237	Sequence 237, App
688	138.5	7.7	639	4	US-08-467-602-241	Sequence 241, App	761	134.5	7.4	647	3	US-08-470-335-243	Sequence 243, App
689	138.5	7.7	639	4	US-08-411-295F-167	Sequence 167, App	762	134.5	7.4	647	3	US-09-009-490A-91	Sequence 91, App1
690	138.5	7.7	648	4	US-08-467-602-253	Sequence 253, App	763	134.5	7.4	647	3	US-08-482-073-5	Sequence 5, App11
691	138.5	7.7	648	4	US-08-411-295F-179	Sequence 179, App	764	134.5	7.4	647	4	US-08-467-602-308	Sequence 308, App
692	138.5	7.7	650	4	US-08-467-602-280	Sequence 280, App	765	134.5	7.4	647	4	US-08-411-295F-234	Sequence 234, App
693	138.5	7.7	650	4	US-08-411-295F-206	Sequence 206, App	766	134.5	7.4	647	5	PT-US93-00031-11	Sequence 11, App1
694	138.5	7.7	653	4	US-08-467-602-275	Sequence 275, App	767	134.5	7.4	647	5	PT-US93-00031-23	Sequence 23, App1
695	138.5	7.7	653	4	US-08-411-295F-201	Sequence 201, App	768	134.5	7.4	652	1	US-08-471-570-10	Sequence 10, App1
696	138.5	7.7	659	4	US-08-467-602-292	Sequence 292, App	769	134.5	7.4	658	4	US-08-467-602-305	Sequence 305, App
697	138.5	7.7	659	4	US-08-411-295F-218	Sequence 218, App	770	134.5	7.4	658	4	US-08-411-295F-231	Sequence 231, App
698	138.5	7.7	662	4	US-08-467-602-289	Sequence 289, App	771	134.5	7.4	667	4	US-08-467-602-314	Sequence 314, App
699	138.5	7.7	662	4	US-08-411-295F-215	Sequence 215, App	772	134.5	7.4	667	4	US-08-411-295F-240	Sequence 240, App
700	138.5	7.7	673	4	US-08-467-602-283	Sequence 283, App	773	134.5	7.4	669	4	US-08-467-602-344	Sequence 344, App
701	138.5	7.7	673	4	US-08-411-295F-209	Sequence 209, App	774	134.5	7.4	669	4	US-08-411-295F-270	Sequence 270, App
702	138.5	7.7	682	4	US-08-467-602-295	Sequence 295, App	775	134.5	7.4	672	4	US-08-467-602-339	Sequence 339, App
703	138.5	7.7	682	4	US-08-411-295F-221	Sequence 221, App	776	134.5	7.4	672	4	US-08-411-295F-285	Sequence 285, App
704	137	7.6	514	4	US-09-949-016-11380	Sequence 11380, A	777	134.5	7.4	678	4	US-08-467-602-353	Sequence 353, App
705	137	7.6	517	4	US-09-723-368-4	Sequence 4, Appli	778	134.5	7.4	678	4	US-08-411-295F-279	Sequence 279, App
706	136.5	7.6	388	1	US-08-445-640-6	Sequence 6, Appli	779	134.5	7.4	681	4	US-08-467-602-350	Sequence 350, App
707	136.5	7.6	388	3	US-08-170-558-6	Sequence 6, Appli	780	134.5	7.4	681	4	US-08-411-295F-276	Sequence 276, App
708	136.5	7.6	388	3	US-08-447-314-6	Sequence 6, Appli	781	134.5	7.4	692	4	US-08-467-602-347	Sequence 347, App
709	136.5	7.6	388	3	US-08-445-461-6	Sequence 6, Appli	782	134.5	7.4	692	4	US-08-411-295F-273	Sequence 273, App
710	136.5	7.6	388	4	US-09-223-490-6	Sequence 6, Appli	783	134.5	7.4	701	4	US-08-467-602-356	Sequence 356, App
711	136.5	7.6	498	4	US-09-354-151-2	Sequence 2, Appli	784	134.5	7.4	701	4	US-08-411-295F-282	Sequence 282, App
712	136.5	7.6	738	3	US-08-478-208-32	Sequence 32, Appl	785	134.5	7.4	740	5	PT-US93-00031-17	Sequence 17, App1
713	136.5	7.6	738	4	US-09-336-536-73	Sequence 73, Appl	786	134.5	7.4	852	3	US-08-470-335-248	Sequence 248, App
714	136.5	7.6	738	6	5264554-2	Patent No. 5264554	787	134.5	7.4	852	4	US-08-467-602-300	Sequence 300, App
715	136.5	7.6	738	6	5264554-2	Patent No. 5264554	788	134.5	7.4	852	4	US-08-411-295F-226	Sequence 226, App
716	136	7.5	393	1	US-08-429-742-2	Sequence 2, Appli	789	134.5	7.4	855	3	US-08-470-335-241	Sequence 241, App
717	136	7.5	458	4	US-09-435-956A-1	Sequence 1, Appli	790	134.5	7.4	855	4	US-08-467-602-298	Sequence 298, App
718	136	7.5	644	5	PT-US93-00031-21	Sequence 21, Appl	791	134.5	7.4	855	4	US-08-411-295F-224	Sequence 224, App
719	135.5	7.5	371	4	US-08-411-295F-308	Sequence 308, App	792	134.5	7.4	861	3	US-08-470-335-251	Sequence 251, App
720	135.5	7.5	405	4	US-08-467-602-384	Sequence 384, App	793	134.5	7.4	861	4	US-08-467-602-312	Sequence 312, App
721	135.5	7.5	405	4	US-08-411-295F-307	Sequence 307, App	794	134.5	7.4	861	4	US-08-411-295F-238	Sequence 238, App
722	135.5	7.5	501	3	US-08-891-845-10	Sequence 10, Appl	795	134.5	7.4	864	3	US-08-470-335-244	Sequence 244, App
723	135.5	7.5	501	4	US-09-514-573-10	Sequence 10, Appl	796	134.5	7.4	864	4	US-08-467-602-309	Sequence 309, App
724	135.5	7.5	768	3	US-08-891-845-2	Sequence 2, Appli	797	134.5	7.4	864	4	US-08-411-295F-235	Sequence 235, App
725	135.5	7.5	768	4	US-09-514-573-2	Sequence 2, Appli	798	134.5	7.4	875	4	US-08-467-602-306	Sequence 306, App
726	135	7.5	492	3	US-08-462-794-11	Sequence 11, Appl	799	134.5	7.4	875	4	US-08-411-295F-232	Sequence 232, App
727	135	7.5	497	4	US-09-499-846-6	Sequence 6, Appli	800	134.5	7.4	884	4	US-08-467-602-315	Sequence 315, App
728	135	7.5	497	4	US-09-499-846-10	Sequence 10, Appl	801	134.5	7.4	884	4	US-08-411-295F-241	Sequence 241, App
729	135	7.5	525	4	US-09-499-846-4	Sequence 4, Appli	802	134.5	7.4	886	4	US-08-467-602-342	Sequence 342, App
730	135	7.5	525	4	US-09-499-846-8	Sequence 8, Appli	803	134.5	7.4	886	4	US-08-411-295F-268	Sequence 268, App
731	134.5	7.4	349	3	US-08-470-335-188	Sequence 188, App	804	134.5	7.4	889	4	US-08-467-602-340	Sequence 340, App
732	134.5	7.4	382	4	US-08-467-602-382	Sequence 382, App	805	134.5	7.4	889	4	US-08-411-295F-266	Sequence 266, App
733	134.5	7.4	434	3	US-09-540-245A-19	Sequence 19, Appl	806	134.5	7.4	895	4	US-08-467-602-354	Sequence 354, App
734	134.5	7.4	456	3	US-08-470-335-246	Sequence 246, App	807	134.5	7.4	895	4	US-08-411-295F-280	Sequence 280, App
735	134.5	7.4	456	4	US-08-467-602-303	Sequence 303, App	808	134.5	7.4	898	4	US-08-467-602-351	Sequence 351, App
736	134.5	7.4	456	4	US-08-411-295F-229	Sequence 229, App	809	134.5	7.4	898	4	US-08-411-295F-277	Sequence 277, App
737	134.5	7.4	459	3	US-08-470-335-239	Sequence 239, App	810	134.5	7.4	899	3	US-08-470-335-249	Sequence 249, App
738	134.5	7.4	459	4	US-08-467-602-299	Sequence 299, App	811	134.5	7.4	899	4	US-08-467-602-301	Sequence 301, App
739	134.5	7.4	459	4	US-08-411-295F-225	Sequence 225, App	812	134.5	7.4	899	4	US-08-411-295F-227	Sequence 227, App
740	134.5	7.4	479	4	US-08-467-602-307	Sequence 307, App	813	134.5	7.4	902	3	US-08-470-335-242	Sequence 242, App
741	134.5	7.4	479	4	US-08-411-295F-233	Sequence 233, App	814	134.5	7.4	902	4	US-08-467-602-296	Sequence 296, App
742	134.5	7.4	490	4	US-08-467-602-345	Sequence 345, App	815	134.5	7.4	902	4	US-08-411-295F-222	Sequence 222, App
743	134.5	7.4	490	4	US-08-411-295F-271	Sequence 271, App	816	134.5	7.4	908	3	US-08-470-335-252	Sequence 252, App
744	134.5	7.4	493	4	US-08-467-602-341	Sequence 341, App	817	134.5	7.4	908	4	US-08-467-602-313	Sequence 313, App
745	134.5	7.4	493	4	US-08-411-295F-267	Sequence 267, App	818	134.5	7.4	908	4	US-08-411-295F-239	Sequence 239, App
746	134.5	7.4	513	4	US-08-467-602-349	Sequence 349, App	819	134.5	7.4	909	4	US-08-467-602-348	Sequence 348, App
747	134.5	7.4	513	4	US-08-411-295F-275	Sequence 275, App	820	134.5	7.4	909	4	US-08-411-295F-274	Sequence 274, App
748	134.5	7.4	526	1	US-08-471-570-4	Sequence 4, Appli	821	134.5	7.4	911	3	US-08-470-335-245	Sequence 245, App
749	134.5	7.4	534	4	US-09-651-200-24	Sequence 6, Appli	822	134.5	7.4	911	4	US-08-467-602-310	Sequence 310, App
750	134.5	7.4	534	4	US-09-651-200-24	Sequence 24, Appl	823	134.5	7.4	911	4	US-08-411-295F-236	Sequence 236, App
751	134.5	7.4	635	3	US-08-470-335-247	Sequence 247, App	824	134.5	7.4	918	4	US-08-467-602-357	Sequence 357, App
752	134.5	7.4	635	4	US-08-467-602-302	Sequence 302, App	825	134.5	7.4	918	4	US-08-411-295F-283	Sequence 283, App
753	134.5	7.4	635	4	US-08-411-295F-228	Sequence 228, App	826	134.5	7.4	922	4	US-08-467-602-304	Sequence 304, App
754	134.5	7.4	638	3	US-08-470-335-240	Sequence 240, App	827	134.5	7.4	922	4	US-08-411-295F-230	Sequence 230, App
755	134.5	7.4	638	4	US-08-467-602-297	Sequence 297, App	828	134.5	7.4	931	4	US-08-467-602-316	Sequence 316, App
756	134.5	7.4	638	4	US-08-411-295F-223	Sequence 223, App	829	134.5	7.4	931	4	US-08-411-295F-242	Sequence 242, App
757	134.5	7.4	643	5	PT-US93-00031-19	Sequence 19, Appl	830	134.5	7.4	933	4	US-08-467-602-343	Sequence 343, App

831	134.5	7.4	933	4	US-08-411-295F-269	Sequence 269, App	904	131	7.3	1106	4	US-09-866-510-16	Sequence 16, Appl
832	134.5	7.4	936	4	US-08-467-602-338	Sequence 338, App	905	131	7.3	1106	4	US-09-866-510-18	Sequence 18, Appl
833	134.5	7.4	936	4	US-08-411-295F-264	Sequence 264, App	906	131	7.3	1106	4	US-09-866-510-20	Sequence 20, Appl
834	134.5	7.4	942	4	US-08-467-602-355	Sequence 355, App	907	131	7.3	1106	4	US-09-866-510-22	Sequence 22, Appl
835	134.5	7.4	942	4	US-08-411-295F-281	Sequence 281, App	908	131	7.3	1106	5	PCT-US92-00730-2	Sequence 2, Appl
836	134.5	7.4	945	4	US-08-467-602-352	Sequence 352, App	909	131	7.3	1106	5	PCT-US92-00862-2	Sequence 2, Appl
837	134.5	7.4	945	4	US-08-411-295F-278	Sequence 278, App	910	130.5	7.2	298	4	US-09-152-060-76	Sequence 76, Appl
838	134.5	7.4	956	4	US-08-467-602-346	Sequence 346, App	911	130.5	7.2	315	4	US-09-949-016-11121	Sequence 11121, A
839	134.5	7.4	956	4	US-08-411-295F-272	Sequence 272, App	912	130.5	7.2	315	4	US-09-949-016-11122	Sequence 11122, A
840	134.5	7.4	965	4	US-08-467-602-358	Sequence 358, App	913	130.5	7.2	432	3	US-08-477-4608-2	Sequence 2, Appl
841	134.5	7.4	965	4	US-08-411-295F-284	Sequence 284, App	914	130.5	7.2	432	3	US-08-379-516-2	Sequence 2, Appl
842	134	7.4	424	6	5169835-6	Patent No. 5169835	915	130.5	7.2	432	3	US-09-329-916-2	Sequence 2, Appl
843	134	7.4	424	6	5169835-6	Patent No. 5169835	916	130.5	7.2	432	3	US-08-485-372A-2	Sequence 2, Appl
844	133.5	7.4	888	1	US-09-499-846-12	Sequence 12, Appl	917	130.5	7.2	432	3	US-09-409-006A-2	Sequence 2, Appl
845	133.5	7.4	888	1	US-08-445-640-35	Sequence 35, Appl	918	130.5	7.2	432	4	US-08-484-681-2	Sequence 2, Appl
846	133.5	7.4	888	3	US-08-170-558-35	Sequence 35, Appl	919	130.5	7.2	432	4	US-09-766-995-2	Sequence 2, Appl
847	133.5	7.4	888	3	US-08-447-314-35	Sequence 35, Appl	920	130.5	7.2	432	5	PCT-US93-07423-2	Sequence 2, Appl
848	133.5	7.4	888	3	US-08-445-461-35	Sequence 35, Appl	921	130.5	7.2	466	4	US-09-604-107A-8	Sequence 8, Appl
849	133.5	7.4	888	4	US-09-223-490-35	Sequence 35, Appl	922	130.5	7.2	249	4	US-09-336-536-42	Sequence 42, Appl
850	133	7.4	317	4	US-09-684-708A-23	Sequence 23, Appl	923	130	7.2	394	4	US-09-336-536-39	Sequence 39, Appl
851	133	7.4	322	3	US-09-383-586-33	Sequence 33, Appl	924	130	7.2	802	3	US-09-173-151A-33	Sequence 33, Appl
852	133	7.4	322	4	US-09-823-038A-33	Sequence 33, Appl	925	129.5	7.2	728	1	US-07-512-952-4	Sequence 4, Appl
853	133	7.4	323	4	US-09-684-708A-25	Sequence 25, Appl	926	129	7.1	340	3	US-09-188-930-184	Sequence 184, App
854	133	7.4	612	2	US-08-359-705B-8	Sequence 8, Appl	927	129	7.1	340	4	US-09-312-283C-184	Sequence 184, App
855	133	7.4	612	2	US-08-286-846A-8	Sequence 8, Appl	928	129	7.1	417	4	US-09-949-016-6729	Sequence 6729, Ap
856	133	7.4	612	3	US-08-457-880A-8	Sequence 8, Appl	929	129	7.1	456	4	US-09-949-016-7564	Sequence 7564, Ap
857	133	7.4	612	3	US-08-444-622A-8	Sequence 8, Appl	930	128	7.1	341	4	US-09-336-536-28	Sequence 28, Appl
858	133	7.4	612	3	US-08-942-562-8	Sequence 8, Appl	931	128	7.1	370	4	US-09-336-536-28	Sequence 28, Appl
859	133	7.4	612	3	US-09-156-923-8	Sequence 8, Appl	932	128	7.1	483	2	US-08-392-338A-19	Sequence 19, Appl
860	133	7.4	816	4	US-09-949-016-10904	Sequence 10904, A	933	128	7.1	483	2	US-09-166-750-19	Sequence 19, Appl
861	133	7.4	839	2	US-08-359-705B-6	Sequence 6, Appl	934	128	7.1	483	3	US-09-166-093-19	Sequence 19, Appl
862	133	7.4	839	2	US-08-286-846A-6	Sequence 6, Appl	935	128	7.1	483	3	US-09-172-019-19	Sequence 19, Appl
863	133	7.4	839	2	US-08-457-880A-6	Sequence 6, Appl	936	128	7.1	483	3	US-09-166-094-19	Sequence 19, Appl
864	133	7.4	839	3	US-08-444-622A-6	Sequence 6, Appl	937	128	7.1	483	4	US-09-443-213-19	Sequence 19, Appl
865	133	7.4	839	3	US-08-942-562-6	Sequence 6, Appl	938	128	7.1	483	4	US-09-949-016-8574	Sequence 8574, Ap
866	133	7.4	839	3	US-09-156-923-6	Sequence 6, Appl	939	128	7.1	795	4	US-09-949-016-7119	Sequence 7119, Ap
867	133	7.4	850	1	US-08-286-305A-7	Sequence 7, Appl	940	128	7.1	806	3	US-09-383-630-3	Sequence 3, Appl
868	133	7.4	850	2	US-08-441-104A-7	Sequence 7, Appl	941	127.5	7.1	100	4	US-08-411-295F-121	Sequence 121, App
869	133	7.4	850	2	US-08-440-816A-7	Sequence 7, Appl	942	127.5	7.1	206	3	US-08-341-018-2	Sequence 2, Appl
870	133	7.4	850	3	US-09-417-381A-7	Sequence 7, Appl	943	127.5	7.1	206	3	US-08-470-335-190	Sequence 190, App
871	132	7.3	387	3	US-09-175-928-2	Sequence 2, Appl	944	127.5	7.1	206	3	US-08-470-339-190	Sequence 190, App
872	132	7.3	408	3	US-09-724-864-62	Sequence 62, Appl	945	127.5	7.1	206	4	US-08-467-602-383	Sequence 383, App
873	131.5	7.3	312	4	US-09-254-465A-9	Sequence 9, Appl	946	127.5	7.1	206	4	US-08-411-295F-2	Sequence 2, Appl
874	131.5	7.3	312	4	US-09-907-794A-64	Sequence 64, Appl	947	127.5	7.1	206	4	US-08-411-295F-76	Sequence 76, Appl
875	131.5	7.3	312	4	US-09-905-125A-64	Sequence 64, Appl	948	127.5	7.1	241	4	US-08-411-295F-94	Sequence 94, Appl
876	131.5	7.3	312	4	US-09-902-775A-64	Sequence 64, Appl	949	127.5	7.1	431	3	US-09-038-832-2	Sequence 2, Appl
877	131.5	7.3	312	4	US-09-906-700-64	Sequence 64, Appl	950	127.5	7.1	431	3	US-09-038-832-2	Sequence 2, Appl
878	131.5	7.3	312	4	US-09-903-603A-64	Sequence 64, Appl	951	127.5	7.1	447	4	US-09-949-016-8211	Sequence 8211, Ap
879	131.5	7.3	312	4	US-09-904-920A-64	Sequence 64, Appl	952	127	7.0	383	4	US-09-949-016-11050	Sequence 11050, A
880	131.5	7.3	312	4	US-09-909-064-64	Sequence 64, Appl	953	127	7.0	992	1	US-07-813-593-2	Sequence 2, Appl
881	131.5	7.3	312	4	US-09-905-381A-64	Sequence 64, Appl	954	127	7.0	992	1	US-07-877-451-2	Sequence 2, Appl
882	131.5	7.3	312	4	US-09-906-618-64	Sequence 64, Appl	955	127	7.0	992	1	US-07-946-507-2	Sequence 2, Appl
883	131.5	7.3	312	4	US-09-953-499-9	Sequence 9, Appl	956	127	7.0	992	1	US-08-252-517-2	Sequence 2, Appl
884	131	7.3	240	1	US-08-471-570-12	Sequence 12, Appl	957	127	7.0	992	1	US-07-906-397A-2	Sequence 2, Appl
885	131	7.3	342	4	US-09-684-708A-27	Sequence 27, Appl	958	127	7.0	992	1	US-08-601-891-2	Sequence 2, Appl
886	131	7.3	561	4	US-09-866-510-24	Sequence 24, Appl	959	127	7.0	992	1	US-09-021-324-2	Sequence 2, Appl
887	131	7.3	782	4	US-09-684-708A-21	Sequence 21, Appl	960	127	7.0	992	4	US-09-872-136B-2	Sequence 2, Appl
888	131	7.3	1090	4	US-09-866-510-14	Sequence 14, Appl	961	127	7.0	992	5	PCT-US92-02750-2	Sequence 2, Appl
889	131	7.3	1106	1	US-08-180-195-2	Sequence 2, Appl	962	127	7.0	992	5	PCT-US92-05401-2	Sequence 2, Appl
890	131	7.3	1106	3	US-08-168-917-2	Sequence 2, Appl	963	127	7.0	992	5	PCT-US92-09893-2	Sequence 2, Appl
891	131	7.3	1106	1	US-08-477-329-2	Sequence 2, Appl	964	126.5	7.0	365	2	US-08-979-424-3	Sequence 3, Appl
892	131	7.3	1106	2	US-08-475-458-2	Sequence 2, Appl	965	126.5	7.0	365	3	US-09-272-496-2	Sequence 2, Appl
893	131	7.3	1106	2	US-08-460-510-2	Sequence 2, Appl	966	126.5	7.0	365	4	US-09-949-016-6064	Sequence 6064, Ap
894	131	7.3	1106	2	US-08-460-490-2	Sequence 2, Appl	967	126	7.0	277	4	US-09-354-151-3	Sequence 3, Appl
895	131	7.3	1106	3	US-08-980-400-2	Sequence 2, Appl	968	126	7.0	477	2	US-08-359-705B-4	Sequence 4, Appl
896	131	7.3	1106	3	US-08-462-728-4	Sequence 4, Appl	969	126	7.0	477	2	US-08-286-846A-4	Sequence 4, Appl
897	131	7.3	1106	3	US-09-583-459A-2	Sequence 2, Appl	970	126	7.0	477	3	US-08-457-880A-4	Sequence 4, Appl
898	131	7.3	1106	3	US-09-583-210-2	Sequence 2, Appl	971	126	7.0	477	3	US-08-444-622A-4	Sequence 4, Appl
899	131	7.3	1106	3	US-09-583-449A-2	Sequence 2, Appl	972	126	7.0	477	3	US-08-942-562-4	Sequence 4, Appl
900	131	7.3	1106	3	US-09-435-059-2	Sequence 2, Appl	973	126	7.0	477	3	US-09-156-923-4	Sequence 4, Appl
901	131	7.3	1106	3	US-08-461-917-4	Sequence 4, Appl	974	126	7.0	822	2	US-08-359-705B-2	Sequence 2, Appl
902	131	7.3	1106	4	US-08-464-436-4	Sequence 4, Appl	975	126	7.0	822	2	US-08-286-846A-2	Sequence 2, Appl
903	131	7.3	1106	4	US-08-464-436-4	Sequence 4, Appl	976	126	7.0	822	2	US-08-457-880A-2	Sequence 2, Appl

977	126	7.0	822	3	US-08-444-622A-2	Sequence 2, Appli	1050	123	6.8	821	1	US-08-339-578-2	Sequence 2, Appli
978	126	7.0	822	3	US-08-942-562-2	Sequence 2, Appli	1051	122.5	6.8	133	4	US-08-467-602-380	Sequence 380, App
979	126	7.0	822	3	US-09-156-923-2	Sequence 2, Appli	1052	122.5	6.8	161	1	US-08-096-277-18	Sequence 18, Appl
980	126	7.0	822	3	US-09-949-016-6698	Sequence 6698, Ap	1053	122.5	6.8	161	2	US-08-550-815-18	Sequence 18, Appl
981	126	7.0	847	1	US-08-286-305A-5	Sequence 5, Appli	1054	122.5	6.8	161	3	US-08-703-089-18	Sequence 18, Appl
982	126	7.0	847	2	US-08-441-104A-5	Sequence 5, Appli	1055	122.5	6.8	207	4	US-08-467-602-219	Sequence 219, App
983	126	7.0	847	2	US-08-440-816A-5	Sequence 5, Appli	1056	122.5	6.8	207	4	US-08-411-295F-145	Sequence 145, App
984	126	7.0	847	3	US-09-417-381A-5	Sequence 5, Appli	1057	122.5	6.8	210	4	US-08-467-602-215	Sequence 215, App
985	126	7.0	1000	1	US-08-222-299-2	Sequence 2, Appli	1058	122.5	6.8	210	4	US-08-411-295F-141	Sequence 141, App
986	126	7.0	1000	2	US-08-434-878-2	Sequence 2, Appli	1059	122.5	6.8	230	4	US-08-467-602-223	Sequence 223, App
987	126	7.0	1000	5	PCT-US95-03718-2	Sequence 2, Appli	1060	122.5	6.8	230	4	US-08-411-295F-149	Sequence 149, App
988	125.5	6.9	365	3	US-08-928-383B-2	Sequence 2, Appli	1061	122.5	6.8	241	4	US-08-467-602-261	Sequence 261, App
989	125.5	6.9	518	4	US-09-919-172-20	Sequence 20, Appli	1062	122.5	6.8	241	4	US-08-411-295F-187	Sequence 187, App
990	125.5	6.9	526	4	US-09-910-174B-9	Sequence 9, Appli	1063	122.5	6.8	241	4	US-08-467-602-257	Sequence 257, App
991	125.5	6.9	526	4	US-09-620-461-9	Sequence 9, Appli	1064	122.5	6.8	244	4	US-08-411-295F-183	Sequence 183, App
992	125.5	6.9	526	4	US-09-949-016-6122	Sequence 6122, Ap	1065	122.5	6.8	264	4	US-08-467-602-265	Sequence 265, App
993	125.5	6.9	540	4	US-09-949-016-11644	Sequence 11644, A	1066	122.5	6.8	264	4	US-08-411-295F-191	Sequence 191, App
994	125.5	6.9	589	2	US-08-724-394A-1	Sequence 1, Appli	1067	122.5	6.8	386	4	US-08-467-602-218	Sequence 218, App
995	125	6.9	391	5	PCT-US95-15696-2	Sequence 2, Appli	1068	122.5	6.8	386	4	US-08-411-295F-144	Sequence 144, App
996	124.5	6.9	241	3	US-08-341-018-54	Sequence 54, Appl	1069	122.5	6.8	389	4	US-08-467-602-213	Sequence 213, App
997	124.5	6.9	241	3	US-08-470-335-195	Sequence 195, App	1070	122.5	6.8	389	4	US-08-411-295F-139	Sequence 139, App
998	124.5	6.9	241	3	US-08-470-339-195	Sequence 195, App	1071	122.5	6.8	395	4	US-08-467-602-227	Sequence 227, App
999	124.5	6.9	241	4	US-08-467-602-389	Sequence 389, App	1072	122.5	6.8	395	4	US-08-411-295F-153	Sequence 153, App
1000	124.5	6.9	241	4	US-08-411-295F-47	Sequence 47, Appl	1073	122.5	6.8	398	4	US-08-467-602-224	Sequence 224, App
1001	124.5	6.9	731	1	US-08-070-165F-10	Sequence 10, Appl	1074	122.5	6.8	398	4	US-08-411-295F-150	Sequence 150, App
1002	124.5	6.9	731	2	US-08-885-418-10	Sequence 10, Appl	1075	122.5	6.8	409	4	US-08-467-602-221	Sequence 221, App
1003	124	6.9	198	4	US-09-569-611C-34	Sequence 34, Appl	1076	122.5	6.8	409	4	US-08-411-295F-147	Sequence 147, App
1004	124	6.9	637	4	US-09-569-611C-35	Sequence 35, Appl	1077	122.5	6.8	418	4	US-08-467-602-230	Sequence 230, App
1005	124	6.9	993	1	US-07-977-451-4	Sequence 4, Appli	1078	122.5	6.8	418	4	US-08-411-295F-156	Sequence 156, App
1006	124	6.9	993	1	US-08-252-517-4	Sequence 4, Appli	1079	122.5	6.8	420	4	US-08-467-602-260	Sequence 260, App
1007	124	6.9	993	1	US-07-906-397A-4	Sequence 4, Appli	1080	122.5	6.8	420	4	US-08-411-295F-186	Sequence 186, App
1008	124	6.9	993	1	US-08-601-891-4	Sequence 4, Appli	1081	122.5	6.8	422	3	US-08-753-007A-9	Sequence 9, Appl1
1009	124	6.9	993	2	US-09-021-324-4	Sequence 4, Appli	1082	122.5	6.8	422	3	US-09-398-496-9	Sequence 9, Appl1
1010	124	6.9	993	4	US-09-872-136B-4	Sequence 4, Appli	1083	122.5	6.8	423	4	US-08-467-602-255	Sequence 255, App
1011	124	6.9	993	5	PCT-US92-09893-4	Sequence 4, Appli	1084	122.5	6.8	423	4	US-08-411-295F-181	Sequence 181, App
1012	124	6.9	999	1	US-08-252-626A-2	Sequence 2, Appli	1085	122.5	6.8	429	4	US-08-467-602-269	Sequence 269, App
1013	124	6.9	999	1	US-09-949-016-6718	Sequence 6718, Ap	1086	122.5	6.8	432	4	US-08-411-295F-195	Sequence 195, App
1014	124	6.9	1160	5	PCT-US92-05401-4	Sequence 4, Appli	1087	122.5	6.8	432	4	US-08-467-602-266	Sequence 266, App
1015	123.5	6.8	156	4	US-08-467-602-381	Sequence 381, App	1088	122.5	6.8	432	4	US-08-411-295F-192	Sequence 192, App
1016	123.5	6.8	156	4	US-08-411-295F-306	Sequence 306, App	1089	122.5	6.8	432	4	US-08-467-602-263	Sequence 263, App
1017	123.5	6.8	241	1	US-07-847-743B-30	Sequence 30, Appl	1090	122.5	6.8	443	4	US-08-411-295F-189	Sequence 189, App
1018	123.5	6.8	241	1	US-08-456-201-30	Sequence 30, Appl	1091	122.5	6.8	452	4	US-08-467-602-272	Sequence 272, App
1019	123.5	6.8	241	2	US-08-456-241-30	Sequence 30, Appl	1092	122.5	6.8	452	4	US-08-411-295F-198	Sequence 198, App
1020	123.5	6.8	241	5	PCT-US92-04295A-30	Sequence 30, Appl	1093	122.5	6.8	603	4	US-08-467-602-216	Sequence 216, App
1021	123.5	6.8	420	1	US-07-847-743B-29	Sequence 29, Appl	1094	122.5	6.8	603	4	US-08-411-295F-142	Sequence 142, App
1022	123.5	6.8	420	1	US-08-456-201-29	Sequence 29, Appl	1095	122.5	6.8	606	4	US-08-467-602-214	Sequence 214, App
1023	123.5	6.8	420	2	US-08-456-241-29	Sequence 29, Appl	1096	122.5	6.8	606	4	US-08-411-295F-140	Sequence 140, App
1024	123.5	6.8	420	5	PCT-US92-04295A-29	Sequence 29, Appl	1097	122.5	6.8	612	4	US-08-467-602-228	Sequence 228, App
1025	123.5	6.8	637	1	US-07-847-743B-28	Sequence 28, Appl	1098	122.5	6.8	612	4	US-08-411-295F-154	Sequence 154, App
1026	123.5	6.8	637	1	US-08-456-201-28	Sequence 28, Appl	1099	122.5	6.8	615	4	US-08-467-602-225	Sequence 225, App
1027	123.5	6.8	637	2	US-08-456-241-28	Sequence 28, Appl	1100	122.5	6.8	615	4	US-08-411-295F-151	Sequence 151, App
1028	123.5	6.8	637	5	PCT-US92-04295A-28	Sequence 28, Appl	1101	122.5	6.8	625	1	US-07-847-743B-26	Sequence 26, Appl
1029	123.5	6.8	645	1	US-07-847-743B-27	Sequence 27, Appl	1102	122.5	6.8	625	2	US-08-456-201-26	Sequence 26, Appl
1030	123.5	6.8	645	1	US-08-456-201-27	Sequence 27, Appl	1103	122.5	6.8	625	2	US-08-456-241-26	Sequence 26, Appl
1031	123.5	6.8	645	1	US-08-428-926-4	Sequence 4, Appli	1104	122.5	6.8	625	5	PCT-US92-04295A-26	Sequence 26, Appl
1032	123.5	6.8	645	1	US-08-428-927-4	Sequence 4, Appli	1105	122.5	6.8	626	4	US-08-467-602-222	Sequence 222, App
1033	123.5	6.8	645	1	US-08-428-298-4	Sequence 4, Appli	1106	122.5	6.8	626	4	US-08-411-295F-148	Sequence 148, App
1034	123.5	6.8	645	1	US-08-339-517-4	Sequence 4, Appli	1107	122.5	6.8	635	4	US-08-467-602-231	Sequence 231, App
1035	123.5	6.8	645	2	US-08-456-241-27	Sequence 27, Appl	1108	122.5	6.8	635	4	US-08-411-295F-157	Sequence 157, App
1036	123.5	6.8	645	3	US-09-020-880-93	Sequence 93, Appl	1109	122.5	6.8	637	4	US-08-467-602-258	Sequence 258, App
1037	123.5	6.8	645	3	US-09-101-544-93	Sequence 93, Appl	1110	122.5	6.8	637	4	US-08-411-295F-184	Sequence 184, App
1038	123.5	6.8	645	4	US-09-097-681-3	Sequence 3, Appli	1111	122.5	6.8	640	4	US-08-467-602-256	Sequence 256, App
1039	123.5	6.8	645	5	PCT-US92-04295A-27	Sequence 27, Appl	1112	122.5	6.8	640	4	US-08-411-295F-182	Sequence 182, App
1040	123.5	6.8	732	1	US-07-847-743B-9	Sequence 9, Appli	1113	122.5	6.8	645	3	US-08-753-007A-10	Sequence 10, Appl
1041	123.5	6.8	732	1	US-08-456-201-9	Sequence 9, Appli	1114	122.5	6.8	645	3	US-09-398-496-10	Sequence 10, Appl
1042	123.5	6.8	732	2	US-08-456-241-9	Sequence 9, Appli	1115	122.5	6.8	646	4	US-08-467-602-270	Sequence 270, App
1043	123.5	6.8	732	5	PCT-US92-04295A-9	Sequence 9, Appli	1116	122.5	6.8	646	4	US-08-411-295F-196	Sequence 196, App
1044	123	6.8	321	4	US-09-254-465A-2	Sequence 2, Appli	1117	122.5	6.8	649	4	US-08-467-602-267	Sequence 267, App
1045	123	6.8	354	6	5169835-4	Sequence 2, Appli	1118	122.5	6.8	649	4	US-08-411-295F-193	Sequence 193, App
1046	123	6.8	354	6	5169835-4	Patent No. 5169835	1119	122.5	6.8	650	4	US-08-467-602-217	Sequence 217, App
1047	123	6.8	553	2	US-08-263-911-9	Sequence 9, Appli	1120	122.5	6.8	650	4	US-08-411-295F-143	Sequence 143, App
1048	123	6.8	553	2	US-08-263-911-9	Sequence 9, Appli	1121	122.5	6.8	653	4	US-08-467-602-212	Sequence 212, App
1049	123	6.8	668	3	US-09-173-151A-35	Sequence 35, Appl	1122	122.5	6.8	653	4	US-08-411-295F-138	Sequence 138, App

1123	122.5	6.8	659	4	US-08-467-602-229	Sequence 229, App	1196	119.5	6.6	197	3	US-08-833-488B-28	Sequence 28, Appl
1124	122.5	6.8	659	4	US-08-411-295F-155	Sequence 155, App	1197	119.5	6.6	253	3	US-08-833-488B-20	Sequence 20, Appl
1125	122.5	6.8	659	4	US-08-467-602-264	Sequence 264, App	1198	119.5	6.6	450	4	US-09-907-794A-320	Sequence 320, App
1126	122.5	6.8	660	4	US-08-411-295F-190	Sequence 190, App	1199	119.5	6.6	450	4	US-09-905-125A-320	Sequence 320, App
1127	122.5	6.8	662	4	US-08-467-602-226	Sequence 226, App	1200	119.5	6.6	450	4	US-09-902-775A-320	Sequence 320, App
1128	122.5	6.8	662	4	US-08-411-295F-152	Sequence 152, App	1201	119.5	6.6	450	4	US-09-906-700-320	Sequence 320, App
1129	122.5	6.8	669	1	US-07-847-743B-8	Sequence 8, Appl	1202	119.5	6.6	450	4	US-09-903-603A-320	Sequence 320, App
1130	122.5	6.8	669	1	US-07-847-743B-13	Sequence 13, Appl	1203	119.5	6.6	450	4	US-09-904-920A-320	Sequence 320, App
1131	122.5	6.8	669	1	US-08-456-201-13	Sequence 8, Appl	1204	119.5	6.6	450	4	US-09-909-064-320	Sequence 320, App
1132	122.5	6.8	669	1	US-08-456-201-13	Sequence 11, Appl	1205	119.5	6.6	450	4	US-09-905-381A-320	Sequence 320, App
1133	122.5	6.8	669	2	US-08-330-161-11	Sequence 11, Appl	1206	119.5	6.6	450	4	US-09-906-618-320	Sequence 320, App
1134	122.5	6.8	669	2	US-08-456-241-8	Sequence 8, Appl	1207	119.5	6.6	477	4	US-09-949-016-9192	Sequence 9192, Ap
1135	122.5	6.8	669	2	US-08-456-241-13	Sequence 13, Appl	1208	119.5	6.6	477	4	US-09-949-016-9193	Sequence 9193, Ap
1136	122.5	6.8	669	2	US-08-440-401-11	Sequence 11, Appl	1209	119.5	6.6	477	4	US-09-949-016-9194	Sequence 9194, Ap
1137	122.5	6.8	669	2	US-08-419-878B-11	Sequence 11, Appl	1210	119.5	6.6	477	4	US-09-949-016-9195	Sequence 9195, Ap
1138	122.5	6.8	669	3	US-08-173-480-11	Sequence 11, Appl	1211	119.5	6.6	477	4	US-09-949-016-9196	Sequence 9196, Ap
1139	122.5	6.8	669	4	US-08-467-602-273	Sequence 273, App	1212	119.5	6.6	477	4	US-09-949-016-9197	Sequence 9197, Ap
1140	122.5	6.8	669	4	US-08-411-295F-199	Sequence 199, App	1213	119.5	6.6	477	4	US-09-949-016-9198	Sequence 9198, Ap
1141	122.5	6.8	669	5	PCT-US92-04295A-8	Sequence 8, Appl	1214	119.5	6.6	477	4	US-09-949-016-9199	Sequence 9199, Ap
1142	122.5	6.8	669	5	PCT-US92-04295A-13	Sequence 13, Appl	1215	119.5	6.6	505	3	US-09-240-915-3	Sequence 3, Appl
1143	122.5	6.8	673	4	US-08-467-602-220	Sequence 220, App	1216	119.5	6.6	505	3	US-09-899-634C-2	Sequence 2, Appl
1144	122.5	6.8	673	4	US-08-411-295F-146	Sequence 146, App	1217	119.5	6.6	261	4	US-08-525-864A-4	Sequence 4, Appl
1145	122.5	6.8	682	4	US-08-467-602-232	Sequence 232, App	1218	119.5	6.6	330	2	US-08-525-864A-4	Sequence 4, Appl
1146	122.5	6.8	682	4	US-08-411-295F-158	Sequence 158, App	1219	119.5	6.6	365	4	US-08-525-864A-2	Sequence 2, Appl
1147	122.5	6.8	684	4	US-08-467-602-259	Sequence 259, App	1220	119.5	6.6	754	2	US-08-525-864A-2	Sequence 2, Appl
1148	122.5	6.8	684	4	US-08-411-295F-185	Sequence 185, App	1221	119.5	6.6	910	4	US-09-313-942-28	Sequence 28, Appl
1149	122.5	6.8	687	4	US-08-467-602-254	Sequence 254, App	1222	119.5	6.6	969	4	US-09-949-016-8059	Sequence 8059, Ap
1150	122.5	6.8	687	4	US-08-411-295F-180	Sequence 180, App	1223	118.5	6.6	533	2	US-08-463-911-7	Sequence 7, Appl
1151	122.5	6.8	693	4	US-08-467-602-271	Sequence 271, App	1224	118.5	6.6	668	4	US-09-949-016-8139	Sequence 8139, Ap
1152	122.5	6.8	693	4	US-08-411-295F-197	Sequence 197, App	1225	118.5	6.6	2860	2	US-08-826-267-2	Sequence 2, Appl
1153	122.5	6.8	696	4	US-08-467-602-268	Sequence 268, App	1226	118.5	6.5	300	1	US-07-640-029-5	Sequence 5, Appl
1154	122.5	6.8	696	4	US-08-411-295F-194	Sequence 194, App	1227	118.5	6.5	300	1	US-08-439-992A-5	Sequence 5, Appl
1155	122.5	6.8	707	4	US-08-467-602-262	Sequence 262, App	1228	118.5	6.5	933	1	US-08-222-299-4	Sequence 4, Appl
1156	122.5	6.8	707	4	US-08-411-295F-188	Sequence 188, App	1229	118.5	6.5	933	2	US-08-434-878-4	Sequence 4, Appl
1157	122.5	6.8	716	4	US-08-467-602-274	Sequence 274, App	1230	118.5	6.5	933	5	PCT-US95-03718-4	Sequence 4, Appl
1158	122.5	6.8	716	4	US-08-411-295F-200	Sequence 200, App	1231	117.5	6.5	191	4	US-09-270-767-33678	Sequence 33678, A
1159	122.5	6.8	716	4	US-09-270-767-33187	Sequence 33187, A	1232	117.5	6.5	191	4	US-09-270-767-48895	Sequence 48895, A
1160	122.5	6.8	357	4	US-09-949-016-9074	Sequence 9074, A	1233	117.5	6.5	246	4	US-09-336-536-31	Sequence 31, Appl
1161	122.5	6.8	363	4	US-09-949-016-11040	Sequence 11040, A	1234	117.5	6.5	336	1	US-07-904-073-2	Sequence 2, Appl
1162	122.5	6.8	365	4	US-09-949-016-9075	Sequence 9075, Ap	1235	117.5	6.5	336	1	US-08-442-043A-16	Sequence 16, Appl
1163	122.5	6.8	371	4	US-09-569-611C-36	Sequence 36, Appl	1236	117.5	6.5	336	1	US-08-441-893A-16	Sequence 16, Appl
1164	122.5	6.8	421	4	US-09-398-496-8	Sequence 8, Appl	1237	117.5	6.5	336	4	US-09-336-536-40	Sequence 40, Appl
1165	122.5	6.8	469	3	US-09-398-496-8	Sequence 8, Appl	1238	117.5	6.5	365	1	US-07-821-716-2	Sequence 2, Appl
1166	122.5	6.8	469	3	US-09-398-496-8	Sequence 32, Appl	1239	117.5	6.5	569	1	US-08-381-603-2	Sequence 2, Appl
1167	122.5	6.8	647	3	US-08-753-007A-32	Sequence 32, Appl	1240	117.5	6.5	569	3	US-08-824-376-2	Sequence 2, Appl
1168	122.5	6.8	647	3	US-09-398-496-32	Sequence 32, Appl	1241	117.5	6.5	569	3	US-08-685-212-2	Sequence 2, Appl
1169	121.5	6.7	231	1	US-08-168-091A-4	Sequence 4, Appl	1242	117.5	6.5	569	3	US-09-173-151A-31	Sequence 31, Appl
1170	121.5	6.7	286	4	US-09-270-767-44618	Sequence 44618, A	1243	117.5	6.5	569	4	US-08-466-932A-2	Sequence 2, Appl
1171	121.5	6.7	390	2	US-08-979-424-1	Sequence 1, Appl	1244	117.5	6.5	569	4	US-08-406-824A-6	Sequence 6, Appl
1172	121.5	6.7	390	4	US-09-907-794A-39	Sequence 39, Appl	1245	117.5	6.5	569	4	US-09-949-016-6000	Sequence 6000, Ap
1173	121.5	6.7	390	4	US-09-905-125A-39	Sequence 39, Appl	1246	117.5	6.5	569	5	PCT-US94-02414-2	Sequence 2, Appl
1174	121.5	6.7	390	4	US-09-902-775A-39	Sequence 39, Appl	1247	117.5	6.5	569	5	PCT-US96-08899-2	Sequence 2, Appl
1175	121.5	6.7	390	4	US-09-906-700-39	Sequence 39, Appl	1248	117.5	6.5	569	5	US-09-949-016-8572	Sequence 8572, Ap
1176	121.5	6.7	390	4	US-09-903-603A-39	Sequence 39, Appl	1249	117.5	6.5	588	4	US-09-270-767-33115	Sequence 33115, A
1177	121.5	6.7	390	4	US-09-904-920A-39	Sequence 39, Appl	1250	117.5	6.5	264	4	US-09-270-767-48332	Sequence 48332, A
1178	121.5	6.7	390	4	US-09-909-064-39	Sequence 39, Appl	1251	117.5	6.5	264	4	US-08-753-007A-6	Sequence 6, Appl
1179	121.5	6.7	390	4	US-09-905-381A-39	Sequence 39, Appl	1252	117.5	6.5	407	3	US-09-398-496-6	Sequence 6, Appl
1180	121.5	6.7	390	4	US-09-906-618-39	Sequence 39, Appl	1253	117.5	6.5	407	3	US-09-131-648-2	Sequence 2, Appl
1181	121.5	6.7	302	1	US-07-921-807B-7	Sequence 7, Appl	1254	117.5	6.5	708	3	US-09-907-794A-69	Sequence 69, Appl
1182	121.5	6.7	302	1	US-08-441-944A-7	Sequence 7, Appl	1255	117.5	6.5	708	4	US-09-905-125A-69	Sequence 69, Appl
1183	121.5	6.7	315	4	US-09-910-174B-28	Sequence 28, Appl	1256	117.5	6.5	708	4	US-09-902-775A-69	Sequence 69, Appl
1184	121.5	6.7	315	4	US-09-620-461-28	Sequence 28, Appl	1257	117.5	6.5	708	4	US-09-906-700-69	Sequence 69, Appl
1185	120.5	6.7	165	1	US-08-168-091A-33	Sequence 33, Appl	1258	117.5	6.5	708	4	US-09-903-603A-69	Sequence 69, Appl
1186	120.5	6.7	197	3	US-08-833-488B-4	Sequence 4, Appl	1259	117.5	6.5	708	4	US-09-904-920A-69	Sequence 69, Appl
1187	120.5	6.7	197	3	US-08-833-488B-9	Sequence 9, Appl	1260	117.5	6.5	708	4	US-09-909-064-69	Sequence 69, Appl
1188	120.5	6.7	236	6	5455030-7	Patent No. 5455030	1261	117.5	6.5	708	4	US-09-905-381A-69	Sequence 69, Appl
1189	120.5	6.7	236	6	5455030-7	Patent No. 5455030	1262	117.5	6.5	708	4	US-09-906-618-69	Sequence 69, Appl
1190	120.5	6.6	193	4	US-09-397-243D-4	Sequence 4, Appl	1263	117.5	6.5	729	1	US-07-640-029-3	Sequence 3, Appl
1191	120.5	6.6	205	3	US-09-462-270-4	Sequence 4, Appl	1264	117.5	6.5	733	1	US-07-640-029-4	Sequence 4, Appl
1192	120.5	6.6	328	4	US-09-949-016-6428	Sequence 6428, Ap	1265	117.5	6.5	733	1	US-07-921-807B-6	Sequence 6, Appl
1193	120.5	6.6	329	4	US-09-149-476-483	Sequence 483, App	1266	117.5	6.5	733	1	US-08-441-944A-6	Sequence 6, Appl
1194	120.5	6.6	332	4	US-09-949-016-7327	Sequence 7327, Ap	1267	117.5	6.5	733	3	US-08-439-992A-4	Sequence 4, Appl
1195	120.5	6.6	361	4	US-09-270-767-45128	Sequence 45128, A	1268	117.5	6.5	733	3		

1269	117	6.5	825	1	US-07-912-952-2	Sequence 2, Appli	Sequence 2, Appli	1342	112.5	6.2	414	4	US-10-697-263-14	Sequence 14, Appl
1270	117	6.5	885	1	US-08-372-892-4	Sequence 4, Appli	Sequence 4, Appli	1343	112.5	6.2	503	4	US-08-999-689A-6	Sequence 6, Appli
1271	117	6.5	885	4	US-09-919-497-52	Sequence 52, Appl	Sequence 52, Appl	1344	112.5	6.2	503	4	US-09-944-807-4	Sequence 4, Appli
1272	117	6.5	894	1	US-08-372-892-2	Sequence 2, Appli	Sequence 2, Appli	1345	112	6.2	170	4	US-09-245-764-6	Sequence 6, Appli
1273	117	6.5	894	1	US-08-445-640-34	Sequence 34, Appl	Sequence 34, Appl	1346	112	6.2	181	3	US-08-753-007A-4	Sequence 4, Appli
1274	117	6.5	894	3	US-08-170-558-34	Sequence 34, Appl	Sequence 34, Appl	1347	112	6.2	181	3	US-09-398-496-4	Sequence 4, Appli
1275	117	6.5	894	3	US-08-447-314-34	Sequence 34, Appl	Sequence 34, Appl	1348	112	6.2	247	6	5455030-9	Patent No. 5455030
1276	117	6.5	894	3	US-08-445-461-34	Sequence 34, Appl	Sequence 34, Appl	1349	112	6.2	247	6	5455030-9	Patent No. 5455030
1277	117	6.5	894	3	US-09-223-490-34	Sequence 34, Appl	Sequence 34, Appl	1350	112	6.2	605	3	US-08-753-007A-2	Sequence 2, Appli
1278	117	6.5	975	4	US-09-949-016-7595	Sequence 7595, Ap	Sequence 7595, Ap	1351	112	6.2	605	3	US-08-753-007A-2	Sequence 2, Appli
1279	117	6.5	1665	4	US-09-858-664A-2	Sequence 2, Appli	Sequence 2, Appli	1352	111.5	6.2	94	2	US-09-398-496-2	Sequence 30, Appl
1280	117	6.5	1665	4	US-10-274-978-2	Sequence 2, Appli	Sequence 2, Appli	1353	111.5	6.2	94	2	US-08-427-497B-35	Sequence 35, Appl
1281	117	6.5	1665	4	US-10-697-263-2	Sequence 2, Appli	Sequence 2, Appli	1354	111.5	6.2	284	4	US-08-961-309-70	Sequence 70, Appl
1282	116.5	6.5	307	2	US-08-332-562A-83	Sequence 83, Appl	Sequence 83, Appl	1355	111.5	6.2	431	4	US-09-773-877B-27	Sequence 27, Appl
1283	116.5	6.5	315	4	US-09-949-016-7014	Sequence 7014, Ap	Sequence 7014, Ap	1356	111.5	6.2	458	4	US-09-773-877B-26	Sequence 26, Appl
1284	116.5	6.5	680	3	US-08-227-496C-15	Sequence 15, Appl	Sequence 15, Appl	1357	111.5	6.2	480	2	US-08-425-989B-11	Sequence 11, Appl
1285	116.5	6.5	1060	4	US-09-419-788-19	Sequence 19, Appl	Sequence 19, Appl	1358	111.5	6.2	567	3	US-09-560-639-7	Sequence 7, Appli
1286	116	6.4	199	3	US-08-833-488B-14	Sequence 14, Appl	Sequence 14, Appl	1359	111.5	6.2	567	3	US-09-173-151A-24	Sequence 24, Appl
1287	116	6.4	731	1	US-07-921-807B-5	Sequence 5, Appli	Sequence 5, Appli	1360	111.5	6.2	567	4	US-09-032-337-39	Sequence 39, Appl
1288	116	6.4	731	1	US-08-441-944A-5	Sequence 5, Appli	Sequence 5, Appli	1361	111	6.1	275	3	US-08-463-903-6	Sequence 6, Appli
1289	116	6.4	731	3	US-08-439-992A-3	Sequence 3, Appli	Sequence 3, Appli	1362	111	6.1	275	3	US-08-463-903-8	Sequence 8, Appli
1290	116	6.4	879	1	US-08-554-612C-1	Sequence 1, Appli	Sequence 1, Appli	1363	111	6.1	275	3	US-07-935-695-6	Sequence 6, Appli
1291	116	6.4	993	1	US-08-183-211-2	Sequence 2, Appli	Sequence 2, Appli	1364	111	6.1	275	3	US-07-935-695-8	Sequence 8, Appli
1292	116	6.4	993	5	PCT-US95-00176A-2	Sequence 2, Appli	Sequence 2, Appli	1365	111	6.1	280	3	US-08-463-903-10	Sequence 10, Appl
1293	115.5	6.4	173	3	US-08-833-488B-31	Sequence 31, Appl	Sequence 31, Appl	1366	111	6.1	280	3	US-07-935-695-10	Sequence 10, Appl
1294	115.5	6.4	229	3	US-08-833-488B-24	Sequence 24, Appl	Sequence 24, Appl	1367	111	6.1	282	3	US-08-463-903-12	Sequence 12, Appl
1295	115.5	6.4	248	1	US-08-323-445A-6	Sequence 6, Appli	Sequence 6, Appli	1368	111	6.1	282	3	US-07-935-695-12	Sequence 12, Appl
1296	115.5	6.4	248	1	US-08-515-903A-6	Sequence 6, Appli	Sequence 6, Appli	1369	111	6.1	321	3	US-09-361-434-17	Sequence 17, Appl
1297	115.5	6.4	248	5	PCT-US95-12840-6	Sequence 6, Appli	Sequence 6, Appli	1370	111	6.1	321	3	US-09-361-434-22	Sequence 22, Appl
1298	115.5	6.4	530	3	US-08-477-460B-4	Sequence 4, Appli	Sequence 4, Appli	1371	111	6.1	321	3	US-09-635-025-17	Sequence 17, Appl
1299	115.5	6.4	530	3	US-08-379-516-4	Sequence 4, Appli	Sequence 4, Appli	1372	111	6.1	321	3	US-09-635-025-22	Sequence 22, Appl
1300	115.5	6.4	530	3	US-09-329-916-4	Sequence 4, Appli	Sequence 4, Appli	1373	111	6.1	398	1	US-08-091-519-2	Sequence 2, Appli
1301	115.5	6.4	530	3	US-08-485-372A-4	Sequence 4, Appli	Sequence 4, Appli	1374	111	6.1	398	1	US-08-442-043A-2	Sequence 2, Appli
1302	115.5	6.4	530	3	US-09-409-006A-4	Sequence 4, Appli	Sequence 4, Appli	1375	111	6.1	398	3	US-09-173-151A-26	Sequence 26, Appl
1303	115.5	6.4	530	4	US-08-484-681-4	Sequence 4, Appli	Sequence 4, Appli	1376	111	6.1	398	4	US-09-461-908-2	Sequence 2, Appli
1304	115.5	6.4	530	4	US-09-766-995-4	Sequence 4, Appli	Sequence 4, Appli	1377	111	6.1	398	4	US-08-441-893A-2	Sequence 2, Appli
1305	115.5	6.4	530	5	PCT-US93-07422-4	Sequence 4, Appli	Sequence 4, Appli	1378	111	6.1	398	4	US-09-579-845-4	Sequence 4, Appli
1306	115	6.4	318	6	5223394-11	Patent No. 5223394	Patent No. 5223394	1379	111	6.1	398	4	US-08-406-824A-8	Sequence 8, Appli
1307	115	6.4	318	6	5223394-11	Patent No. 5223394	Patent No. 5223394	1380	111	6.1	398	4	US-09-921-667-8	Sequence 8, Appli
1308	114.5	6.3	139	1	US-08-168-091A-35	Sequence 35, Appl	Sequence 35, Appl	1381	111	6.1	398	5	PCT-US91-03478-2	Sequence 2, Appli
1309	114.5	6.3	365	3	US-08-928-383B-23	Sequence 23, Appl	Sequence 23, Appl	1382	111	6.1	418	4	US-09-949-016-9458	Sequence 9458, Ap
1310	114.5	6.3	365	3	US-08-928-383B-24	Sequence 24, Appl	Sequence 24, Appl	1383	111	6.1	418	4	US-08-030-175-41	Sequence 41, Appl
1311	114.5	6.3	455	4	US-09-949-016-6949	Sequence 6949, Ap	Sequence 6949, Ap	1384	111	6.1	467	4	US-08-030-175-42	Sequence 42, Appl
1312	114	6.3	302	1	US-07-640-029-6	Sequence 6, Appli	Sequence 6, Appli	1385	111	6.1	479	4	US-09-723-368-2	Sequence 2, Appli
1313	114	6.3	302	1	US-07-921-807B-8	Sequence 8, Appli	Sequence 8, Appli	1386	111	6.1	479	4	US-09-949-016-6278	Sequence 6278, Ap
1314	114	6.3	302	1	US-08-441-944A-8	Sequence 8, Appli	Sequence 8, Appli	1387	111	6.1	522	4	US-09-949-016-7563	Sequence 7563, Ap
1315	114	6.3	302	3	US-08-439-992A-6	Sequence 6, Appli	Sequence 6, Appli	1388	111	6.1	551	4	US-08-896-537A-2	Sequence 2, Appli
1316	114	6.3	467	3	US-09-046-736-2	Sequence 2, Appli	Sequence 2, Appli	1389	111	6.1	729	1	US-08-070-165B-6	Sequence 6, Appli
1317	113.5	6.3	262	1	US-08-323-445A-4	Sequence 4, Appli	Sequence 4, Appli	1390	111	6.1	729	2	US-08-885-418-6	Sequence 6, Appli
1318	113.5	6.3	262	1	US-08-515-903A-4	Sequence 4, Appli	Sequence 4, Appli	1391	110.5	6.1	141	4	US-09-858-664A-15	Sequence 15, Appl
1319	113.5	6.3	262	5	PCT-US95-12840-4	Sequence 4, Appli	Sequence 4, Appli	1392	110.5	6.1	141	4	US-10-274-978-16	Sequence 16, Appl
1320	113.5	6.3	307	3	US-08-996-338-25	Sequence 25, Appl	Sequence 25, Appl	1393	110.5	6.1	141	4	US-10-697-263-16	Sequence 16, Appl
1321	113.5	6.3	307	4	US-09-556-972-25	Sequence 25, Appl	Sequence 25, Appl	1394	110.5	6.1	260	3	US-08-463-903-2	Sequence 2, Appli
1322	113.5	6.3	455	4	US-09-949-016-11026	Sequence 11026, A	Sequence 11026, A	1395	110.5	6.1	260	3	US-07-935-695-2	Sequence 2, Appli
1323	113.5	6.3	518	3	US-09-240-915-8	Sequence 8, Appli	Sequence 8, Appli	1396	110.5	6.1	260	4	US-08-961-309-64	Sequence 64, Appl
1324	113.5	6.3	518	3	US-09-591-435-8	Sequence 8, Appli	Sequence 8, Appli	1397	110.5	6.1	275	3	US-08-463-903-17	Sequence 17, Appl
1325	113.5	6.3	519	3	US-08-996-338-21	Sequence 21, Appl	Sequence 21, Appl	1398	110.5	6.1	275	3	US-07-935-695-17	Sequence 17, Appl
1326	113.5	6.3	537	1	US-09-556-972-21	Sequence 21, Appl	Sequence 21, Appl	1399	110.5	6.1	584	4	US-09-910-174B-16	Sequence 16, Appl
1327	113.5	6.3	537	1	US-08-604-333-4	Sequence 4, Appli	Sequence 4, Appli	1400	110.5	6.1	584	4	US-09-620-461-16	Sequence 16, Appl
1328	113.5	6.3	537	3	US-09-110-618-4	Sequence 4, Appli	Sequence 4, Appli	1401	110.5	6.1	601	2	US-08-795-868-16	Sequence 16, Appl
1329	113.5	6.3	537	3	US-09-173-151A-29	Sequence 29, Appl	Sequence 29, Appl	1402	110.5	6.1	602	3	US-09-303-069-16	Sequence 16, Appl
1330	113.5	6.3	537	4	US-09-578-178-4	Sequence 4, Appli	Sequence 4, Appli	1403	110.5	6.1	602	3	US-09-134-250-16	Sequence 16, Appl
1331	113.5	6.3	537	4	US-09-577-806-4	Sequence 4, Appli	Sequence 4, Appli	1404	110.5	6.1	640	4	US-09-907-794A-292	Sequence 292, App
1332	113.5	6.3	537	4	US-09-621-502-8	Sequence 8, Appli	Sequence 8, Appli	1405	110.5	6.1	640	4	US-09-905-125A-232	Sequence 292, App
1333	113.5	6.3	547	1	US-08-473-981A-6	Sequence 6, Appli	Sequence 6, Appli	1406	110.5	6.1	640	4	US-09-902-775A-292	Sequence 292, App
1334	113.5	6.3	547	2	US-08-474-087-6	Sequence 6, Appli	Sequence 6, Appli	1407	110.5	6.1	640	4	US-09-906-700-292	Sequence 292, App
1335	113	6.3	273	4	US-09-270-767-32843	Sequence 32843, A	Sequence 32843, A	1408	110.5	6.1	640	4	US-09-903-603A-292	Sequence 292, App
1336	113	6.3	273	4	US-09-270-767-42060	Sequence 42060, A	Sequence 42060, A	1409	110.5	6.1	640	4	US-09-904-920A-232	Sequence 292, App
1337	113	6.3	278	4	US-09-270-767-42034	Sequence 42034, A	Sequence 42034, A	1410	110.5	6.1	640	4	US-09-909-064-292	Sequence 292, App
1338	113	6.3	458	4	US-09-773-877B-22	Sequence 22, Appl	Sequence 22, Appl	1411	110.5	6.1	640	4	US-09-905-381A-292	Sequence 292, App
1339	112.5	6.2	365	3	US-08-928-383B-26	Sequence 26, Appl	Sequence 26, Appl	1412	110.5	6.1	640	4	US-09-906-618-292	Sequence 292, App
1340	112.5	6.2	414	4	US-09-858-664A-13	Sequence 13, Appl	Sequence 13, Appl	1413	110	6.1	242	2	US-08-224-591-14	Sequence 14, Appl
1341	112.5	6.2	414	4	US-10-274-978-14	Sequence 14, Appl	Sequence 14, Appl	1414	110	6.1	242	2	US-08-392-338A-23	Sequence 23, Appl





```
US-09-700-397-4
; Sequence 4, Application US/09700397
; Patent No. 6664383
; GENERAL INFORMATION:
; APPLICANT: Ono Pharmaceutical Co., Ltd.
; TITLE OF INVENTION: No. 6664383el Polypeptides, cDNA encoding the same, and use of
; FILE REFERENCE: Q61459
; CURRENT APPLICATION NUMBER: US/09/700,397
; CURRENT FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: JP 10-131815
; PRIOR FILING DATE: 1998-05-14
; PRIOR APPLICATION NUMBER: PCT/JP99/02485
; PRIOR FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-700-397-4

Query Match          90.9%; Score 1642; DB 4; Length 313;
Best Local Similarity 100.0%; Pred. No. 7.6e-156;
Matches 313; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 RSGDATPPKAMDNTVVRQGESATLRCTIDNRVTRVAWLNRSSTILYAGNDKWCLDPRVLL 91
Db 1 RSGDATPPKAMDNTVVRQGESATLRCTIDNRVTRVAWLNRSSTILYAGNDKWCLDPRVLL 60

Qy 92 SNTQTOYSIEIQNVDDVDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGN 151
Db 61 SNTQTOYSIEIQNVDDVDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGN 120

Qy 152 NISLTCIATGRPEPTVTRHISPKAVGFVSEDEYLEIQGITREQSGDYECASNDVAAPV 211
Db 121 NISLTCIATGRPEPTVTRHISPKAVGFVSEDEYLEIQGITREQSGDYECASNDVAAPV 180

Qy 212 VRRVKVTNVPYPISEAKGTGVPVGOKGTLOCEASAVPSAEFQYKDDKRLIEGKGKV 271
Db 181 VRRVKVTNVPYPISEAKGTGVPVGOKGTLOCEASAVPSAEFQYKDDKRLIEGKGKV 240

Qy 272 ENRPFLSKLFFNVSEHDYGNITCVASNKLGHNTNASIMLFGPGAVSEVSNGTERRAGCVW 331
Db 241 ENRPFLSKLFFNVSEHDYGNITCVASNKLGHNTNASIMLFGPGAVSEVSNGTERRAGCVW 300

Qy 332 LLPLLVHLLKLF 344
Db 301 LLPLLVHLLKLF 313

RESULT 3
US-09-976-594-404
; Sequence 404, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 404
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673549 1640555CD1
US-09-976-594-404
```

```
Query Match          51.6%; Score 931.5; DB 4; Length 338;
Best Local Similarity 55.4%; Pred. No. 1.2e-84;
Matches 180; Conservative 60; Mismatches 80; Indels 5; Gaps 4;

Qy 20 LAALCLLP-OGVPPVRSQDATPPKAMDNTVVRQGESATLRCTIDNRVTRVAWLNRSSTILYAG 78
Db 17 LRLLCLLPGLPVRSD--FNRGTDNITVRQGTALRCLVLEKDKSKVAWLNRSGLIFAG 74

Qy 79 NDXKCLDPRVLLSNTQTOYSIEIQNVDDVDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 75 HDKWSLDPRVELEKRHSLEYSRLIQKVVVDEGTYTCSVQTOHEPKTSQVYLLIVQVPPKI 134

Qy 139 VEISSDISINEGNISLTCIATGRPEPTVTRHISPKAVGFVSEDEYLEIQGITREQSGD 198
Db 135 SNISSDVTNVEGNSVTLVCMANGRPPEVITWRHLTPTGREFEGBEYLEYLTIGITREQSGK 194

Qy 199 YECASNDVAAPVRRVKVTNVPYPISEAKGTGVPVGOKGTLOCEASAVPSAEFQYK 258
Db 195 YECKAANEVSSADVKKQKVTNVPYPIITKESKNEATGROASLKCEASAVPADPFEWYRD 254

Qy 259 DKRLIEGKGKVKNRPFLSKLFFNVSEHDYGNITCVASNKLGHNTNASIMLFGPGAVSE 318
Db 255 DTR-INSANGLEIKSTEGQSSLTVTNVTBHYGNITCVAANKLGVTNASLVLFRPGSVRG 313

Qy 319 VSNGTERRAGCVWLLPLLVHLLK 343
Db 314 I-NGSISLAVPLWLLAASLLCLLSK 337

RESULT 4
US-08-414-657D-42
; Sequence 42, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
```

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-414-657D-43

Query Match      51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.6e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATEPKAMDNVTVRQGESATLRCTIDNRVTRVAMNRSIYAG 78
Db 17 LRLCLLPTGLPVSVD--FNRGTDNITVRQGTAILRCVVDKNSKVAMNRSIIFAG 74
QY 79 NDKWCLDPVRVLLSNTQTQYSIEIQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 75 HDKWSLDPRVLEKRAHLEYSRLQKVDVDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 134
QY 139 VEISSDISINEGNNISITCIATGRPEPTVTRHISPKAVGFVSEDEYLEIGITREOSGD 198
Db 135 SNISSDVTNVEGNNVILVCMANGRPPEVITWRHLTPLGRFEPEGEYLEILGITREOSGK 194
QY 199 YECASNDVAAPVVRVVKVTNYPYISEAKGTGVPVGQKGTLOCEASAVPSAEFQYKD 258
Db 195 YECKAANEVSSADVQKQVTVNYPPTITESKSNEATTGROASLKCEASAVPADFEWYRD 254
QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVANSKLGHTNASIMLFGPGAVSE 318
Db 255 DTR-INSANGLEIKSTEGOSLTVTNVTEEHYGNVTCVANKLGVTNASLVLFRPGSVRG 313
QY 319 VSNGTSSRRAGCVMLLPLVLLHLK 343
Db 314 I-NGSISLAVPLMLLAASLFCLLSK 337

RESULT 5
US-08-414-657D-43
; Sequence 43, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 43:

;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-414-657D-43

Query Match      51.3%; Score 926.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.6e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATEPKAMDNVTVRQGESATLRCTIDNRVTRVAMNRSIYAG 78
Db 17 LRLCLLPTGLPVSVD--FNRGTDNITVRQGTAILRCVVDKNSKVAMNRSIIFAG 74
QY 79 NDKWCLDPVRVLLSNTQTQYSIEIQNVVDVDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 75 HDKWSLDPRVLEKRAHLEYSRLQKVDVDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 134
QY 139 VEISSDISINEGNNISITCIATGRPEPTVTRHISPKAVGFVSEDEYLEIGITREOSGD 198
Db 135 SNISSDVTNVEGNNVILVCMANGRPPEVITWRHLTPLGRFEPEGEYLEILGITREOSGK 194
QY 199 YECASNDVAAPVVRVVKVTNYPYISEAKGTGVPVGQKGTLOCEASAVPSAEFQYKD 258
Db 195 YECKAANEVSSADVQKQVTVNYPPTITESKSNEATTGROASLKCEASAVPADFEWYRD 254
QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVANSKLGHTNASIMLFGPGAVSE 318
Db 255 DTR-INSANGLEIKSTEGOSLTVTNVTEEHYGNVTCVANKLGVTNASLVLFRPGSVRG 313
QY 319 VSNGTSSRRAGCVMLLPLVLLHLK 343
Db 314 I-NGSISLAVPLMLLAASLFCLLSK 337

RESULT 6
US-09-135-080-4
; Sequence 4, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-620-3214
```

```
; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-135-080-4

Query Match 51.3%; Score 926.5; DB 4; Length 338;
Best Local Similarity 55.1%; Pred. No. 3.6e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDTPFKAMDNTVVRQGESATLRCTIDNRVTRVAVLNRSTILYAG 78
Db 17 LRLCLLPTGLPVRSD--FNRGTDNITVRQDGTAILRCVLEDKNSKVAMLRSGIIFAG 74
QY 79 NDKWCLDPRLVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 75 HDKWSLDPRLVELEKRHALESRLRIQKVDVDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 134
QY 139 VEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEIQGITREOSGD 198
Db 135 SNISSDVTNVEGNSVTLVCMANGRPEPVITWRHLTPTGREFEGEEVLEILGITREOSGK 194
QY 199 YECASNDVAAPVRRVKVTNNYPPIYSEAKGTGVPVGQKGTLOCEASAVPSAEFOWYKD 258
Db 195 YECCAANEVSSADVKQKVTNNYPPTITESKSNEATTGROASLKCEASAVPAPDFEYRD 254
QY 259 DKRLIEGKGVKVENRPFSLKIFFNVSEHDYGNVTCVASNKLGHNTNASIMLFGPGAVSE 318
Db 255 DTR-INSANGLEIKSTEGQSSLTNTVTBEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 313
QY 319 VSNGTSSRRAGCVMLLPLLLHLIK 343
Db 314 I-NGSISLAVPLWLLAASLCLLSK 337

RESULT 7
US-08-414-657D-2
; Sequence 2, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135

; TELEFAX: 609-620-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-09-135-080-4

Query Match 51.1%; Score 923.5; DB 2; Length 325;
Best Local Similarity 55.3%; Pred. No. 6.8e-84;
Matches 177; Conservative 60; Mismatches 78; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDTPFKAMDNTVVRQGESATLRCTIDNRVTRVAVLNRSTILYAG 78
Db 10 LRLCLLPTGLPVRSD--FNRGTDNITVRQDGTAILRCVLEDKNSKVAMLRSGIIFAG 67
QY 79 NDKWCLDPRLVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 68 HDKWSLDPRLVELEKRHSLSRLRIQKVDVDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 127
QY 139 VEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEIQGITREOSGD 198
Db 128 SNISSDVTNVEGNSVTLVCMANGRPEPVITWRHLTPTGREFEGEEVLEILGITREOSGK 187
QY 199 YECASNDVAAPVRRVKVTNNYPPIYSEAKGTGVPVGQKGTLOCEASAVPSAEFOWYKD 258
Db 188 YECCAANEVSSADVKQKVTNNYPPTITESKSNEATTGROASLKCEASAVPAPDFEYRD 247
QY 259 DKRLIEGKGVKVENRPFSLKIFFNVSEHDYGNVTCVASNKLGHNTNASIMLFGPGAVSE 318
Db 248 DTR-INSANGLEIKSTEGQSSLTNTVTBEHYGNYTCVAANKLGVTNASLVLFRPGSVRG 306
QY 319 VSNGTSSRRAGCVMLLPLLL 338
Db 307 I-NGSISLAVPLWLLAASLL 325

RESULT 8
US-08-414-657D-41
; Sequence 41, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER:
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MEDIUM TYPE: diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080

Query Match 51.1%; Score 923.5; DB 2; Length 325;
Best Local Similarity 55.3%; Pred. No. 6.8e-84;
Matches 177; Conservative 60; Mismatches 78; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAVLNRSTILYAG 78
DB 10 LRLCLLPTGLPVRSD--FNRGTDNITVRQDGTALRLCVLEDKNSKVAWLNRSGIIFAG 67
QY 79 NDKWCLDPRLVLLSNTQTSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
DB 68 HDKWSLDPRLVLEKRSLEYSRLRIQKVVDYDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 127
QY 139 VEISSDISINEGNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEIQITREOSGD 198
DB 128 SNISSDVTNVEGNSVTLVCMANGRPPEVITWRHLTPTGREFEGEEYLEILGITREOSGK 187
QY 199 YECASNDVAAPVRRVKVTNPPYISBAKGTGVPVGQKGTLCQCEASAVPSAEFOWYKD 258
DB 248 DTR-INSANGLEIKSTEGQSLTNTVTEBHYGNYTCVAANKLGVNTNASILVLFPRGVRG 306
QY 319 VSNGTSSRRACVWLLPLLV 338
DB 307 I-NGSISLAVPLMLLAASLL 325

RESULT 9
US-09-135-080-2
; Sequence 2, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080

; APPLICATION NUMBER:
; FILING DATE: 17-AUG-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/414,657
; FILING DATE: 31-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102A
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MEDIUM TYPE: diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,080

Query Match 51.1%; Score 923.5; DB 2; Length 325;
Best Local Similarity 55.3%; Pred. No. 6.8e-84;
Matches 177; Conservative 60; Mismatches 78; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAVLNRSTILYAG 78
DB 10 LRLCLLPTGLPVRSD--FNRGTDNITVRQDGTALRLCVLEDKNSKVAWLNRSGIIFAG 67
QY 79 NDKWCLDPRLVLLSNTQTSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
DB 68 HDKWSLDPRLVLEKRSLEYSRLRIQKVVDYDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 127
QY 139 VEISSDISINEGNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEIQITREOSGD 198
DB 128 SNISSDVTNVEGNSVTLVCMANGRPPEVITWRHLTPTGREFEGEEYLEILGITREOSGK 187
QY 199 YECASNDVAAPVRRVKVTNPPYISBAKGTGVPVGQKGTLCQCEASAVPSAEFOWYKD 258
DB 248 DTR-INSANGLEIKSTEGQSLTNTVTEBHYGNYTCVAANKLGVNTNASILVLFPRGVRG 306
QY 319 VSNGTSSRRACVWLLPLLV 338
DB 307 I-NGSISLAVPLMLLAASLL 325

RESULT 10
US-08-414-657D-60
; Sequence 60, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
```

```
;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
;
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-414-657D-60

Query Match 51.1%; Score 923.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 7.3e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATFPKAMDNVTVRQGSATLRCTIDNRVTRVAVLNRSSTLYAG 78
DB 17 LRLCLLPTGLPVRSD--FNRGTDNITVRQGTAILRCVLEDKNSKVAWLNRSGIIFAG 74
QY 79 NDKWCLEDPVRLVLSNTQYISIEIQNVVDYDEGPYTCVQTDNHPKTSRVHLIVQVSPKI 138
DB 75 HDKWSLEDPVRLVLEKRSLSLRQKVDVDEGSYTCVQTDHPKTSQVYLLIVQVPPKI 134
QY 139 VEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLETQITRQSGD 198
DB 135 SNISSDVTNVEGNSVTLVCMANGRPPEVITWRHLPTGTREFEGBEEYLEILGITRQSGK 194
QY 199 YECASNDVAAPVRRVKVTNNYPPISEAKGTGVPVGQKGLQCEASAVPSAEFQWYKD 258
DB 195 YECKAANEVSSADVQKQVTVNYPPTITESKSNEATTGRQASLKCEASAVPADFEWYRD 254
QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNKLGHNTNASIMLFGPGAVSE 318
DB 255 DTR-INSANGLEIKSTEGQSSLTVTWVTEEHYGNITCVAAKLGVTNASLVLPFGSVRG 313
QY 319 VNSGTSRRAGCVMLPLLVHLHLK 343
DB 314 I-NGSISLAVPLMLLAASLLCLLSK 337

RESULT 11
US-09-135-080-8
; Sequence 8, Application US/09135080
; Patent No. 6423827
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat R.
; APPLICANT: Pimenta, Aurea
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA

;
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
;
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-414-657D-60

Query Match 51.1%; Score 923.5; DB 2; Length 338;
Best Local Similarity 55.1%; Pred. No. 7.3e-84;
Matches 179; Conservative 60; Mismatches 81; Indels 5; Gaps 4;

QY 20 LAALCLF-QGVPRSGDATFPKAMDNVTVRQGSATLRCTIDNRVTRVAVLNRSSTLYAG 78
DB 17 LRLCLLPTGLPVRSD--FNRGTDNITVRQGTAILRCVLEDKNSKVAWLNRSGIIFAG 74
QY 79 NDKWCLEDPVRLVLSNTQYISIEIQNVVDYDEGPYTCVQTDNHPKTSRVHLIVQVSPKI 138
DB 75 HDKWSLEDPVRLVLEKRSLSLRQKVDVDEGSYTCVQTDHPKTSQVYLLIVQVPPKI 134
QY 139 VEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLETQITRQSGD 198
DB 135 SNISSDVTNVEGNSVTLVCMANGRPPEVITWRHLPTGTREFEGBEEYLEILGITRQSGK 194
QY 199 YECASNDVAAPVRRVKVTNNYPPISEAKGTGVPVGQKGLQCEASAVPSAEFQWYKD 258
DB 195 YECKAANEVSSADVQKQVTVNYPPTITESKSNEATTGRQASLKCEASAVPADFEWYRD 254
QY 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNITCVASNKLGHNTNASIMLFGPGAVSE 318
DB 255 DTR-INSANGLEIKSTEGQSSLTVTWVTEEHYGNITCVAAKLGVTNASLVLPFGSVRG 313
QY 319 VNSGTSRRAGCVMLPLLVHLHLK 343
DB 314 I-NGSISLAVPLMLLAASLLCLLSK 337

RESULT 12
US-08-414-657D-46
; Sequence 46, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
```

```
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 308 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-414-657D-46

Query Match 50.3%; Score 908; DB 2; Length 308;
Best Local Similarity 56.3%; Pred. No. 2.2e-82;
Matches 170; Conservative 58; Mismatches 70; Indels 4; Gaps 3;

Qy 20 LAALCLF-QGVPRVSGDATFPKAMDNVTVRQGSATLRCTIDNRVTRVAMNRSSTLYAG 78
Db 10 LRLCLLPTGLPVRSD--FNRGTDNITVRQGTALRLCVLEKSKVAMNRSGLIFAG 67
Qy 79 NDKWCLDPRLVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 68 HDKWSLDPRVELEKRSLSRLQKVDYDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 127
Qy 139 VEISSDISINEGNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEITQITREOSGD 198
Db 128 SNISSDVTNVEGNSVTLVCMANGRPEPVITWRHLTPTRGFEFEGEEYLEITGITREOSGK 187
Qy 199 YECASNDVAAPVRRVKVTNYPPISEAKGTGVPVGQGTGLQCEASAVPSAEFOWYKD 258
Db 188 YECCAANEVSSADVQKVTVNYPPTITESKSNEATTGROASLKCEASAVPADDFEYRD 247
Qy 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVANSKLGHTNASTMLFGPGAVSE 318
Db 248 DTR-INSANGLEIKSTEGQSSLTVTNVTTEHYGNYTCVAANKLGVTNASTMLFRPGSVRG 306
Qy 319 VS 320
Db 307 IN 308

RESULT 13
US-08-414-657D-47
; Sequence 47, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
; TITLE OF INVENTION: Limbic System-Associated Membrane
; TITLE OF INVENTION: Protein and DNA
; NUMBER OF SEQUENCES: 60
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 997 Lenox Drive, Building 3, Suite 210
; CITY: Lawrenceville
; STATE: NJ
; COUNTRY: USA
; ZIP: 08543
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/414,657D
; FILING DATE: 31-MAR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Bloom, Allen
; REGISTRATION NUMBER: 29,135
; REFERENCE/DOCKET NUMBER: 317743-102
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-520-3214
; TELEFAX: 609-520-3259
; TELEX:
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 315 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-414-657D-47

Query Match 50.2%; Score 907; DB 2; Length 315;
Best Local Similarity 56.3%; Pred. No. 2.9e-82;
Matches 170; Conservative 58; Mismatches 70; Indels 4; Gaps 3;

Qy 20 LAALCLF-QGVPRVSGDATFPKAMDNVTVRQGSATLRCTIDNRVTRVAMNRSSTLYAG 78
Db 17 LRLCLLPTGLPVRSD--FNRGTDNITVRQGTALRLCVLEKSKVAMNRSGLIFAG 74
Qy 79 NDKWCLDPRLVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTDNHPKTSRVHLIVQVSPKI 138
Db 75 HDKWSLDPRVELEKRSLSRLQKVDYDEGPTCSVQTDNHPKTSRVHLIVQVPPKI 134
Qy 139 VEISSDISINEGNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEITQITREOSGD 198
Db 135 SNISSDVTNVEGNSVTLVCMANGRPEPVITWRHLTPTRGFEFEGEEYLEITGITREOSGK 194
Qy 199 YECASNDVAAPVRRVKVTNYPPISEAKGTGVPVGQGTGLQCEASAVPSAEFOWYKD 258
Db 195 YECCAANEVSSADVQKVTVNYPPTITESKSNEATTGROASLKCEASAVPADDFEYRD 254
Qy 259 DKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVANSKLGHTNASTMLFGPGAVSE 318
Db 255 DTR-INSANGLEIKSTEGQSSLTVTNVTTEHYGNYTCVAANKLGVTNASTMLFRPGSVRG 313
Qy 319 VS 320
Db 314 IN 315

RESULT 14
US-08-414-657D-45
; Sequence 45, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
; APPLICANT: Pimenta, Aurea
; APPLICANT: Fischer, Itzhak
; APPLICANT: Zhukareva, Victoria
```

```
;; TITLE OF INVENTION: Limbic System-Associated Membrane
;; TITLE OF INVENTION: Protein and DNA
;; NUMBER OF SEQUENCES: 60
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dechert Price & Rhoads
;; STREET: 997 Lenox Drive, Building 3, Suite 210
;; CITY: Lawrenceville
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 08543
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/414,657D
;; FILING DATE: 31-MAR-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bloom, Allen
;; REGISTRATION NUMBER: 29,135
;; REFERENCE/DOCKET NUMBER: 317743-102
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 609-520-3214
;; TELEFAX: 609-520-3259
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 45:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 310 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-414-657D-45
```

```
Query Match 50.1%; Score 905; DB 2; Length 310;
Best Local Similarity 55.3%; Pred. No. 4.5e-82;
Matches 173; Conservative 59; Mismatches 77; Indels 4; Gaps 3;

Qy 31 VRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSITLYAGNDKWCCLDPRVVL 90
Db 1 VRSDV--FNRGTDNITVRQGDITAILRCVLEDKNSKVAWLNRSGLIFAGHDKWSLDPRVEL 58

Qy 91 LSNQTQOYSIEIQNVVDYDEGPTYCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEG 150
Db 59 EKRAHLEYSLRIOKVVDYDEGSYTCVQTOHEPKTSQVYLIVQVPPKISNISSDVTVNEG 118

Qy 151 NNISLTCIATGRPEPTVTRWHISPKAVGFVSEDEYLEIOGITREQSGDYECASNDVAAP 210
Db 119 SNVTLVCMANGREPEPTVTRWHLTPGREFEGEBEYLEILGITREQSGKYECKAANEVSSA 178

Qy 211 VVRVKVTVNYPPYVISEAKGTGVPVQKGTLOCEASAVPSAEQWYKDKRLIEGKKGVK 270
Db 179 DVQKVVTVNYPPPTTESKNEATTGQASLKCEASAVPADPEWYRDDTR-INSANGLE 237

Qy 271 VNRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTASIMLFGGAVSEVSNGTSTRAGCV 330
Db 238 IKSTEGOSSLTVTNVTSEHYGNTYCAANKLGVNTNASLVLFRPGSVRGI-NGSISLAVPL 296

Qy 331 WLLPLLVLHLLK 343
Db 297 WLLAASLFCLLSK 309
```

RESULT 15

```
US-08-414-657D-44
; Sequence 44, Application US/08414657D
; Patent No. 5861283
; GENERAL INFORMATION:
; APPLICANT: Levitt, Pat
```

```
;; APPLICANT: Pimenta, Aurea
;; APPLICANT: Fischer, Itzhak
;; APPLICANT: Zhukareva, Victoria
;; TITLE OF INVENTION: Limbic System-Associated Membrane
;; TITLE OF INVENTION: Protein and DNA
;; NUMBER OF SEQUENCES: 60
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dechert Price & Rhoads
;; STREET: 997 Lenox Drive, Building 3, Suite 210
;; CITY: Lawrenceville
;; STATE: NJ
;; COUNTRY: USA
;; ZIP: 08543
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/414,657D
;; FILING DATE: 31-MAR-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bloom, Allen
;; REGISTRATION NUMBER: 29,135
;; REFERENCE/DOCKET NUMBER: 317743-102
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 609-520-3214
;; TELEFAX: 609-520-3259
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 44:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 304 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
US-08-414-657D-44
```

```
Query Match 49.9%; Score 902; DB 2; Length 304;
Best Local Similarity 55.5%; Pred. No. 8.7e-82;
Matches 171; Conservative 59; Mismatches 74; Indels 4; Gaps 3;

Qy 31 VRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSITLYAGNDKWCCLDPRVVL 90
Db 1 VRSDV--FNRGTDNITVRQGDITAILRCVLEDKNSKVAWLNRSGLIFAGHDKWSLDPRVEL 58

Qy 91 LSNQTQOYSIEIQNVVDYDEGPTYCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEG 150
Db 59 EKRAHLEYSLRIOKVVDYDEGSYTCVQTOHEPKTSQVYLIVQVPPKISNISSDVTVNEG 118

Qy 151 NNISLTCIATGRPEPTVTRWHISPKAVGFVSEDEYLEIOGITREQSGDYECASNDVAAP 210
Db 119 SNVTLVCMANGREPEPTVTRWHLTPGREFEGEBEYLEILGITREQSGKYECKAANEVSSA 178

Qy 211 VVRVKVTVNYPPYVISEAKGTGVPVQKGTLOCEASAVPSAEQWYKDKRLIEGKKGVK 270
Db 179 DVQKVVTVNYPPPTTESKNEATTGQASLKCEASAVPADPEWYRDDTR-INSANGLE 237

Qy 271 VNRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTASIMLFGGAVSEVSNGTSTRAGCV 330
Db 238 IKSTEGOSSLTVTNVTSEHYGNTYCAANKLGVNTNASLVLFRPGSVRGI-NGSISLAVPL 296

Qy 331 WLLPLLVL 338
Db 297 WLLAASLL 304
```

```
Search completed: October 19, 2005, 16:27:56
Job time : 33 secs
```



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 19, 2005, 16:28:12 ; Search time 168 Seconds

(without alignments)  
853.511 Million cell updates/sec

Perfect score: 1806

Sequence: 1 MKTIQPMHNSISWAIFTGL.....RRAGCVMLPLLVHLLKLF 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1860064 seqs, 416830855 residues

Total number of hits satisfying chosen parameters: 1860064

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
- 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
52	1806	100.0	344	14	US-10-066-269-104
64	1806	100.0	344	14	US-10-167-749-523
226	1806	100.0	344	14	US-10-223-085-56
232	1806	100.0	344	14	US-10-219-065-126
262	1806	100.0	344	14	US-10-223-084-56
263	1806	100.0	344	14	US-10-223-088-56
264	1806	100.0	344	14	US-10-223-090-56
269	1806	100.0	344	14	US-10-223-087-56
271	1806	100.0	344	14	US-10-223-089-56
274	1806	100.0	344	14	US-10-223-089-56
447	1806	100.0	344	14	US-10-223-081-56
485	1806	100.0	344	14	US-10-223-082-56
52	1806	100.0	344	14	US-10-066-269-104
64	1806	100.0	344	14	US-10-167-749-523
226	1806	100.0	344	14	US-10-223-085-56
232	1806	100.0	344	14	US-10-219-065-126
262	1806	100.0	344	14	US-10-223-084-56
263	1806	100.0	344	14	US-10-223-088-56
264	1806	100.0	344	14	US-10-223-090-56
269	1806	100.0	344	14	US-10-223-087-56
271	1806	100.0	344	14	US-10-223-089-56
274	1806	100.0	344	14	US-10-223-089-56
447	1806	100.0	344	14	US-10-223-081-56
485	1806	100.0	344	14	US-10-223-082-56

554	1806	100.0	344	15	US-10-170-481A-523	Sequence 523, App
556	1806	100.0	344	15	US-10-210-028-523	Sequence 523, App
615	1806	100.0	344	15	US-10-162-521A-523	Sequence 523, App
623	1806	100.0	344	15	US-10-305-654-56	Sequence 56, Appl
635	1806	100.0	344	15	US-10-657-103-3	Sequence 3, Appl
639	1806	100.0	344	15	US-10-081-056-56	Sequence 56, Appl
658	1806	100.0	344	17	US-10-918-851-523	Sequence 523, App
659	1806	100.0	344	17	US-10-931-886-376	Sequence 376, App
660	1806	100.0	344	17	US-10-805-667-523	Sequence 523, App
661	1806	100.0	344	17	US-10-897-359-523	Sequence 523, App
663	1806	100.0	344	17	US-10-893-802-523	Sequence 523, App
664	1806	100.0	344	17	US-10-897-360-523	Sequence 523, App
665	1806	100.0	344	18	US-10-955-952-376	Sequence 376, App
667	1799	99.6	344	9	US-09-966-546-4	Sequence 4, Appl
668	1799	99.6	344	9	US-09-966-546-6	Sequence 6, Appl
669	1799	99.6	344	9	US-09-966-545-4	Sequence 4, Appl
670	1799	99.6	344	9	US-09-966-545-6	Sequence 6, Appl
671	1799	99.6	344	10	US-09-965-212-4	Sequence 4, Appl
672	1799	99.6	344	10	US-09-965-212-6	Sequence 6, Appl
673	1799	99.6	344	14	US-10-189-940-4	Sequence 4, Appl
674	1799	99.6	344	14	US-10-189-940-6	Sequence 6, Appl
675	1799	99.6	344	18	US-10-971-479-4	Sequence 4, Appl
676	1799	99.6	344	18	US-10-971-479-6	Sequence 6, Appl
677	1665.5	92.2	344	14	US-10-161-572-50	Sequence 50, Appl
678	1665.5	92.2	344	15	US-10-295-027-456	Sequence 456, App
679	1650	91.4	355	14	US-10-306-133-1	Sequence 1, Appl
680	1642	90.9	313	15	US-10-657-103-4	Sequence 4, Appl
681	1639.5	90.8	344	14	US-10-306-133-3	Sequence 3, Appl
682	1427.5	79.0	344	15	US-10-015-115-87	Sequence 87, Appl
683	1295	71.7	250	16	US-10-311-823-15	Sequence 15, Appl
684	1285.5	71.2	338	15	US-10-015-115-86	Sequence 86, Appl
685	1268	70.2	345	14	US-10-161-572-59	Sequence 59, Appl
686	1268	70.2	345	15	US-10-015-115-84	Sequence 84, Appl
687	1268	70.2	345	17	US-10-696-639-46	Sequence 46, Appl
688	1266	70.1	345	15	US-10-015-115-83	Sequence 83, Appl
689	1259	69.7	345	15	US-10-015-115-85	Sequence 85, Appl
690	938.5	52.0	338	15	US-10-038-854-159	Sequence 159, App
691	931.5	51.6	338	9	US-09-808-602-69	Sequence 69, Appl
692	931.5	51.6	338	10	US-09-800-198-58	Sequence 58, Appl
693	931.5	51.6	338	14	US-10-161-572-58	Sequence 58, Appl
694	931.5	51.6	338	15	US-10-038-854-158	Sequence 158, App
695	931.5	51.6	338	15	US-10-042-865-92	Sequence 92, Appl
696	930.5	51.5	350	9	US-09-808-602-71	Sequence 71, Appl
697	930.5	51.5	350	10	US-09-800-198-60	Sequence 60, Appl
698	926.5	51.3	338	9	US-09-808-602-72	Sequence 72, Appl
699	926.5	51.3	338	10	US-09-800-198-61	Sequence 61, Appl
700	926.5	51.3	338	15	US-10-042-865-91	Sequence 91, Appl
701	893	49.4	383	10	US-09-978-418-38	Sequence 38, Appl
702	893	49.4	383	17	US-10-485-231-38	Sequence 38, Appl
703	873.5	48.4	203	15	US-10-187-975-108	Sequence 108, App
704	852.5	47.2	326	14	US-10-106-698-5794	Sequence 5794, App
705	842	46.6	352	15	US-10-038-854-156	Sequence 156, App
706	842	46.6	352	15	US-10-042-865-89	Sequence 89, Appl
713	823	45.6	354	14	US-10-066-269-130	Sequence 130, App
823	45.6	354	14	US-10-219-065-2	Sequence 2, Appl	
817	823	45.6	354	15	US-10-038-854-24	Sequence 24, Appl
820	823	45.6	354	15	US-10-312-352-15	Sequence 15, Appl
823	822	45.5	354	15	US-10-042-865-14	Sequence 14, Appl
824	820	45.4	354	15	US-10-104-047-2965	Sequence 2965, App
825	819	45.3	354	14	US-10-038-854-26	Sequence 26, Appl
826	815	45.1	348	14	US-10-161-572-56	Sequence 56, Appl
827	815	45.1	348	14	US-10-161-572-57	Sequence 57, Appl
828	815	45.1	348	15	US-10-038-854-155	Sequence 155, App
829	815	45.1	348	15	US-10-042-865-88	Sequence 88, Appl
864	815	45.1	352	14	US-10-167-749-612	Sequence 612, App
900	815	45.1	352	15	US-10-170-481A-612	Sequence 612, App
902	815	45.1	352	15	US-10-210-028-612	Sequence 612, App
907	815	45.1	352	15	US-10-162-521A-612	Sequence 612, App
919	815	45.1	352	17	US-10-918-851-612	Sequence 612, App
920	815	45.1	352	17	US-10-808-667-612	Sequence 612, App
921	815	45.1	352	17	US-10-897-359-612	Sequence 612, App
922	815	45.1	352	17	US-10-893-802-612	Sequence 612, App
923	815	45.1	352	17	US-10-897-360-612	Sequence 612, App

924	763	42.2	336	15	US-10-471-449-9	Sequence 9, Appli	997	260	14.4	1395	20	US-11-097-143-31563	Sequence 31563, A
925	763	42.2	336	16	US-10-480-172-8	Sequence 8, Appli	998	255.5	14.1	1024	18	US-10-737-318-44	Sequence 44, Appl
926	761	42.1	319	15	US-10-015-115-22	Sequence 22, Appl	999	255.5	14.1	1024	18	US-10-737-318-46	Sequence 46, Appl
927	761	42.1	319	15	US-10-015-115-24	Sequence 24, Appl	1000	255	14.1	1024	20	US-11-097-143-18552	Sequence 18552, A
928	757	41.9	307	15	US-10-015-115-26	Sequence 26, Appl	1001	254.5	14.1	5175	15	US-10-120-801-74	Sequence 74, Appl
929	726	40.2	336	15	US-10-332-947-53	Sequence 53, Appl	1002	254.5	14.1	5175	15	US-10-369-493-6859	Sequence 6859, Ap
930	721	39.9	336	15	US-10-015-115-28	Sequence 28, Appl	1003	254.5	14.1	5175	15	US-10-369-493-6861	Sequence 6861, Ap
931	720.5	39.9	281	9	US-09-764-853-561	Sequence 561, App	1004	254.5	14.1	5198	15	US-10-120-801-75	Sequence 75, Appl
932	681.5	37.7	351	15	US-10-332-947-52	Sequence 52, Appl	1005	254.5	14.1	5198	15	US-10-369-493-6858	Sequence 6858, Ap
933	632	35.0	133	13	US-10-378-029-73	Sequence 73, Appl	1006	254.5	14.1	5198	15	US-10-369-493-6860	Sequence 6860, Ap
934	603	33.4	141	18	US-10-450-763-44207	Sequence 44207, A	1007	254.5	14.1	5198	15	US-10-346-863-34	Sequence 34, Appl
935	599	33.2	261	15	US-10-038-854-157	Sequence 157, App	1008	253.5	14.0	404	10	US-09-977-418-24	Sequence 24, Appl
936	599	33.2	261	15	US-10-042-865-90	Sequence 90, Appl	1009	253.5	14.0	404	10	US-09-977-033A-24	Sequence 24, Appl
937	569.5	31.5	130	18	US-10-450-763-44206	Sequence 44206, A	1010	253.5	14.0	404	10	US-09-977-751C-24	Sequence 24, Appl
938	527	29.2	256	16	US-10-480-172-14	Sequence 14, Appl	1011	253.5	14.0	404	10	US-09-977-639A-24	Sequence 24, Appl
939	525.5	29.1	872	18	US-10-450-763-44175	Sequence 44175, A	1012	253.5	14.0	404	11	US-09-977-819B-24	Sequence 24, Appl
940	472	26.1	241	16	US-10-480-172-12	Sequence 12, Appl	1013	253.5	14.0	404	14	US-10-161-572-44	Sequence 44, Appl
941	338.5	18.7	413	20	US-11-097-143-35247	Sequence 35247, A	1014	253	14.0	570	16	US-10-311-823-13	Sequence 13, Appl
942	333	18.4	313	20	US-11-097-143-23718	Sequence 23718, A	1015	253	14.0	586	16	US-10-311-823-7	Sequence 7, Appli
943	308.5	17.1	528	13	US-10-108-605-49	Sequence 49, Appl	1016	250.5	13.9	885	20	US-11-097-143-11298	Sequence 11298, A
944	306	16.9	545	20	US-11-097-143-14514	Sequence 14514, A	1017	250	13.8	374	16	US-10-311-823-16	Sequence 16, Appl
945	297.5	16.5	333	20	US-11-097-143-3633	Sequence 3633, Ap	1018	250	13.8	442	16	US-10-311-823-12	Sequence 12, Appl
946	290.5	16.1	2572	14	US-10-114-153-86	Sequence 86, Appl	1019	250	13.8	458	16	US-10-311-823-4	Sequence 4, Appli
947	290.5	16.1	2673	15	US-10-120-801-76	Sequence 76, Appl	1020	250	13.8	1219	18	US-10-450-763-42459	Sequence 42459, A
948	290.5	16.1	2673	18	US-10-934-998-101	Sequence 101, App	1021	250	13.8	1315	15	US-10-094-886-52	Sequence 52, Appl
949	290.5	16.1	4495	15	US-10-138-588-20	Sequence 20, Appl	1022	250	13.8	1386	15	US-10-094-886-38	Sequence 38, Appl
950	290.5	16.1	5636	14	US-10-032-189-128	Sequence 128, App	1023	249.5	13.8	607	9	US-09-991-326-12	Sequence 12, Appl
951	290.5	16.1	5636	15	US-10-120-801-72	Sequence 72, Appl	1024	249.5	13.8	1040	18	US-10-713-124-10	Sequence 10, Appl
952	290.5	16.1	5636	16	US-10-023-634-93	Sequence 93, Appl	1025	248	13.7	467	20	US-11-097-143-33438	Sequence 33438, A
953	290.5	16.1	5636	15	US-10-408-765A-1895	Sequence 1895, Ap	1026	246.5	13.6	1007	16	US-10-408-765A-118	Sequence 118, App
954	290.5	16.1	5636	18	US-10-934-998-81	Sequence 81, Appl	1027	246.5	13.6	1018	15	US-10-367-978-67	Sequence 67, Appl
955	288.5	16.0	707	15	US-10-138-588-18	Sequence 18, Appl	1028	246.5	13.6	1018	18	US-10-712-124-88	Sequence 88, Appl
956	288.5	16.0	961	15	US-10-162-335-42	Sequence 42, Appl	1029	246.5	13.6	1018	18	US-10-631-467-948	Sequence 948, App
957	288.5	16.0	1240	18	US-10-450-763-34292	Sequence 34292, A	1030	244.5	13.5	512	15	US-10-094-749-2493	Sequence 2493, Ap
958	288.5	16.0	1336	15	US-10-019-065A-33	Sequence 33, Appl	1031	243.5	13.5	605	9	US-09-991-326-8	Sequence 8, Appli
959	288.5	16.0	1902	14	US-10-114-153-88	Sequence 88, Appl	1032	242.5	13.4	792	18	US-10-450-763-33418	Sequence 33418, A
960	288.5	16.0	1933	14	US-10-115-478-89	Sequence 89, Appl	1033	242.5	13.4	893	18	US-10-450-763-30617	Sequence 30617, A
961	288.5	16.0	3643	14	US-10-032-189-127	Sequence 127, App	1034	242.5	13.4	893	18	US-10-450-763-30970	Sequence 30970, A
962	288.5	16.0	3645	20	US-10-120-801-73	Sequence 73, Appl	1035	242	13.4	2586	9	US-09-729-485A-11	Sequence 11, Appl
963	288.5	16.0	4126	20	US-11-049-637-4	Sequence 4, Appli	1036	242	13.4	2586	9	US-09-729-485A-14	Sequence 14, Appl
964	288.5	16.0	5518	20	US-11-049-637-2	Sequence 2, Appli	1037	242	13.4	2586	9	US-09-802-318-11	Sequence 11, Appl
965	288.5	16.0	5622	18	US-10-773-446-128	Sequence 128, App	1038	242	13.4	2586	9	US-09-802-318-14	Sequence 14, Appl
966	288.5	16.0	5635	15	US-10-451-168-78	Sequence 78, Appl	1039	242	13.4	2586	9	US-09-905-129-11	Sequence 11, Appl
967	288.5	16.0	5635	18	US-10-980-387-78	Sequence 78, Appl	1040	242	13.4	2586	9	US-09-905-129-14	Sequence 14, Appl
968	284.5	15.8	467	20	US-11-097-143-15924	Sequence 15924, A	1041	242	13.4	2586	9	US-09-991-630-11	Sequence 11, Appl
969	278.5	15.4	4162	15	US-10-023-634-92	Sequence 92, Appl	1042	242	13.4	2586	15	US-09-991-630-14	Sequence 14, Appl
970	276	15.3	733	15	US-10-094-749-3192	Sequence 3192, Ap	1043	242	13.4	2586	15	US-10-454-351-11	Sequence 11, Appl
971	276	15.3	848	16	US-10-311-509-21	Sequence 21, Appl	1044	242	13.4	2586	15	US-10-454-351-14	Sequence 14, Appl
972	276	15.3	848	17	US-10-482-029-204	Sequence 204, App	1045	242	13.4	2587	9	US-09-729-485A-16	Sequence 16, Appl
973	276	15.3	848	18	US-10-852-335A-113	Sequence 113, App	1046	242	13.4	2587	9	US-09-802-318-16	Sequence 16, Appl
974	276	15.3	848	18	US-10-992-287-48	Sequence 48, Appl	1047	242	13.4	2587	9	US-09-905-129-16	Sequence 16, Appl
975	275.5	15.3	853	18	US-10-496-905-513	Sequence 513, App	1048	242	13.4	2587	9	US-09-991-630-16	Sequence 16, Appl
976	275	15.2	848	14	US-10-207-655-180	Sequence 180, App	1049	242	13.4	2587	15	US-10-454-351-16	Sequence 16, Appl
977	274	15.2	1477	14	US-10-274-583-20	Sequence 20, Appl	1050	242	13.4	2589	9	US-10-454-351-24	Sequence 24, Appl
978	273.5	15.1	1356	15	US-10-085-198-108	Sequence 108, App	1051	242	13.4	2589	15	US-10-454-351-24	Sequence 24, Appl
979	271.5	15.0	1426	15	US-10-085-198-106	Sequence 106, App	1052	241.5	13.4	1020	18	US-10-631-467-1637	Sequence 1637, Ap
980	270	15.0	729	20	US-11-097-143-32490	Sequence 32490, A	1053	241	13.3	891	18	US-10-450-763-37895	Sequence 37895, A
981	269	14.9	152	14	US-10-091-438-168	Sequence 168, App	1054	240	13.3	3707	17	US-10-852-335A-139	Sequence 139, App
982	268.5	14.9	1479	15	US-10-231-956A-325	Sequence 325, App	1055	238.5	13.2	1024	17	US-10-737-318-41	Sequence 41, Appl
983	268.5	14.9	1496	14	US-10-021-660-125	Sequence 125, App	1056	235.5	13.0	2623	15	US-10-454-351-32	Sequence 32, Appl
984	268.5	14.9	1496	15	US-10-331-496A-28	Sequence 28, Appl	1057	235	13.0	662	15	US-10-369-493-6726	Sequence 6726, Ap
985	268.5	14.9	1496	15	US-10-211-462-87	Sequence 87, Appl	1058	232.5	12.9	2783	15	US-10-369-493-6344	Sequence 6344, Ap
986	268.5	14.9	1496	16	US-10-723-860-1721	Sequence 1721, Ap	1059	232	12.8	2591	14	US-10-032-189-56	Sequence 56, Appl
987	268.5	14.9	1496	15	US-10-496-905-616	Sequence 616, App	1060	232	12.8	2617	14	US-10-032-189-46	Sequence 46, Appl
988	268.5	14.9	1498	15	US-10-243-553-899	Sequence 899, App	1061	232	12.8	3931	13	US-10-120-801-18	Sequence 18, Appl
989	268.5	14.9	1498	15	US-10-276-774-1957	Sequence 1957, Ap	1062	230.5	12.8	868	13	US-10-016-283-1	Sequence 1, Appli
990	266	14.7	36946	18	US-10-840-512-155	Sequence 155, App	1063	230	12.7	4393	15	US-10-231-956A-366	Sequence 366, App
991	261	14.5	1395	9	US-09-808-602-67	Sequence 67, Appl	1064	230	12.7	4393	17	US-10-741-600-1105	Sequence 1105, Ap
992	261	14.5	1395	10	US-09-800-198-56	Sequence 56, Appl	1065	230	12.7	4393	18	US-10-450-763-53624	Sequence 53624, A
993	261	14.5	1395	14	US-10-289-776-15	Sequence 15, Appl	1066	229.5	12.7	849	15	US-10-435-751-161	Sequence 161, App
994	261	14.5	1395	17	US-10-826-812-2	Sequence 2, Appli	1067	229.5	12.7	851	15	US-10-435-751-162	Sequence 162, App
995	261	14.5	1395	20	US-11-022-546-15	Sequence 15, Appl	1068	229.5	12.7	869	13	US-10-016-283-33	Sequence 33, Appl
996	260.5	14.4	496	20	US-11-097-143-12948	Sequence 12948, A	1069	229.5	12.7	893	15	US-10-435-751-7	Sequence 7, Appli

1070	229.5	12.7	893	15	US-10-435-751-22	Sequence 22, Appl	1145	224	12.4	1059	9	US-09-905-291A-290	Sequence 290, App
1071	229.5	12.7	893	15	US-10-435-751-160	Sequence 160, App	1213	224	12.4	1059	14	US-10-299-976-290	Sequence 290, App
1072	229.5	12.7	893	15	US-10-435-751-201	Sequence 201, App	1214	224	12.4	1059	14	US-10-299-937-290	Sequence 290, App
1073	229.5	12.7	1117	15	US-10-435-751-9	Sequence 9, Appl	1215	224	12.4	1059	15	US-10-298-993-290	Sequence 290, App
1074	229.5	12.7	1117	15	US-10-435-751-23	Sequence 23, Appl	1216	224	12.4	1059	15	US-10-448-923-290	Sequence 290, App
1075	229.5	12.7	1117	15	US-10-435-751-166	Sequence 166, App	1217	224	12.4	1059	15	US-10-449-656-290	Sequence 290, App
1076	229.5	12.7	1117	15	US-10-435-751-168	Sequence 168, App	1218	224	12.4	1059	15	US-10-448-713-290	Sequence 290, App
1077	229.5	12.7	1117	15	US-10-435-751-202	Sequence 202, App	1219	224	12.4	1059	15	US-10-425-447-290	Sequence 290, App
1078	229.5	12.7	1183	15	US-10-435-751-13	Sequence 13, Appl	1220	224	12.4	1059	16	US-10-215-371-290	Sequence 290, App
1079	229.5	12.7	1183	15	US-10-435-751-25	Sequence 25, Appl	1221	224	12.4	1059	16	US-10-771-187-290	Sequence 290, App
1080	229.5	12.7	1183	15	US-10-435-751-178	Sequence 178, App	1222	224	12.4	1059	17	US-10-963-467-290	Sequence 290, App
1081	229.5	12.7	1183	15	US-10-435-751-180	Sequence 180, App	1223	224	12.4	1059	17	US-10-978-255-290	Sequence 290, App
1082	229.5	12.7	1183	15	US-10-435-751-204	Sequence 204, App	1224	224	12.4	1059	18	US-10-797-362-290	Sequence 290, App
1083	229.5	12.7	1208	15	US-10-435-751-11	Sequence 11, Appl	1225	224	12.4	1059	18	US-10-970-823-290	Sequence 290, App
1084	229.5	12.7	1208	15	US-10-435-751-24	Sequence 24, Appl	1228	224	12.4	1119	9	US-09-905-291A-294	Sequence 294, App
1085	229.5	12.7	1183	15	US-10-435-751-172	Sequence 172, App							
1086	229.5	12.7	1208	15	US-10-435-751-174	Sequence 174, App							
1087	229.5	12.7	1208	15	US-10-435-751-203	Sequence 203, App							
1088	229.5	12.7	1224	15	US-10-435-751-3	Sequence 3, Appl							
1089	229.5	12.7	1224	15	US-10-435-751-19	Sequence 19, Appl							
1090	229.5	12.7	1224	15	US-10-435-751-20	Sequence 20, Appl							
1091	229.5	12.7	1224	15	US-10-435-751-28	Sequence 28, Appl							
1092	229.5	12.7	1224	15	US-10-435-751-29	Sequence 29, Appl							
1093	229.5	12.7	1224	15	US-10-435-751-31	Sequence 31, Appl							
1094	229.5	12.7	1224	15	US-10-435-751-32	Sequence 32, Appl							
1095	229.5	12.7	1224	15	US-10-435-751-33	Sequence 33, Appl							
1096	229.5	12.7	1224	15	US-10-435-751-34	Sequence 34, Appl							
1097	229.5	12.7	1224	15	US-10-435-751-35	Sequence 35, Appl							
1098	229.5	12.7	1224	15	US-10-435-751-126	Sequence 126, App							
1099	229.5	12.7	1224	15	US-10-435-751-155	Sequence 155, App							
1100	229.5	12.7	1224	15	US-10-435-751-167	Sequence 167, App							
1101	229.5	12.7	1224	15	US-10-435-751-173	Sequence 173, App							
1102	229.5	12.7	1224	15	US-10-435-751-179	Sequence 179, App							
1103	229.5	12.7	1224	15	US-10-435-751-185	Sequence 185, App							
1104	229.5	12.7	1224	15	US-10-435-751-191	Sequence 191, App							
1105	229.5	12.7	1224	15	US-10-435-751-196	Sequence 196, App							
1106	229.5	12.7	1224	15	US-10-435-751-197	Sequence 197, App							
1107	229.5	12.7	1224	15	US-10-435-751-198	Sequence 198, App							
1108	229.5	12.7	1224	15	US-10-435-751-199	Sequence 199, App							
1109	229.5	12.7	1224	15	US-10-435-751-208	Sequence 208, App							
1110	229.5	12.7	1224	16	US-10-408-765A-1408	Sequence 1408, Ap							
1111	229	12.7	1056	14	US-10-098-871-65	Sequence 65, Appl							
1112	229	12.7	3588	16	US-10-741-601-378	Sequence 378, App							
1113	229	12.7	3588	17	US-10-741-600-1104	Sequence 1104, Ap							
1114	229	12.7	4346	16	US-10-741-601-377	Sequence 377, App							
1115	229	12.7	4346	17	US-10-741-600-1103	Sequence 1103, Ap							
1116	229	12.7	4347	16	US-10-741-601-376	Sequence 376, App							
1117	229	12.7	4347	17	US-10-741-600-1102	Sequence 1102, Ap							
1118	229	12.7	4370	16	US-10-408-765A-1267	Sequence 1267, Ap							
1119	228	12.6	1483	18	US-10-450-763-46695	Sequence 46695, A							
1120	227.5	12.5	8523	18	US-10-840-512-162	Sequence 162, App							
1121	226	12.5	6642	15	US-10-369-493-5013	Sequence 5013, Ap							
1122	225.5	12.5	869	16	US-10-471-115-18	Sequence 18, Appl							
1123	225	12.5	4391	16	US-10-478-451-1	Sequence 1, Appl							
1124	224.5	12.4	477	15	US-10-613-413A-23	Sequence 23, Appl							
1125	224.5	12.4	477	17	US-10-885-225-23	Sequence 23, Appl							
1126	224.5	12.4	477	17	US-10-954-094-23	Sequence 23, Appl							
1127	224.5	12.4	869	9	US-09-817-487A-2	Sequence 2, Appl							
1128	224.5	12.4	981	18	US-10-450-763-52992	Sequence 52992, A							
1129	224.5	12.4	1171	15	US-10-435-751-5	Sequence 5, Appl							
1130	224.5	12.4	1171	15	US-10-435-751-21	Sequence 21, Appl							
1131	224.5	12.4	1171	15	US-10-435-751-154	Sequence 154, App							
1132	224.5	12.4	1171	15	US-10-435-751-156	Sequence 156, App							
1133	224.5	12.4	1171	15	US-10-435-751-200	Sequence 200, App							
1134	224.5	12.4	1224	16	US-10-435-751-30	Sequence 30, Appl							
1135	224.5	12.4	1224	16	US-10-723-860-2585	Sequence 2585, Ap							
1136	224.5	12.4	1224	18	US-10-756-149-5414	Sequence 5414, Ap							
1137	224.5	12.4	1224	18	US-10-631-467-771	Sequence 771, App							
1138	224.5	12.4	1645	18	US-10-450-763-50367	Sequence 50367, A							
1139	224.5	12.4	1765	18	US-10-450-763-52990	Sequence 52990, A							
1140	224.5	12.4	1944	18	US-10-450-763-42376	Sequence 42376, A							
1141	224	12.4	434	18	US-10-450-763-32476	Sequence 32476, A							
1142	224	12.4	737	18	US-10-450-763-32378	Sequence 32378, A							

Search completed: October 19, 2005, 16:37:39  
Job time : 187 secs

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 19, 2005, 16:27:21 ; Search time 172 Seconds

(without alignments)  
1024.158 Million cell updates/sec

Title: US-09-978-544A-523

Perfect score: 1806

Sequence: 1 MKTIQPKMNSISWAIFTLG.....RRACCVWLLPLLVHLLKF 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

UniProt 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

\*Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1780	98.6	344	2	O8BG33 m mus muscu
2	1665.5	92.2	344	1	NTRI HUMAN
3	1647.5	91.2	344	1	NTRI MOUSE
4	1639.5	90.8	344	1	NTRI RAT
5	1477.5	81.8	353	1	CEPU CHICK
6	1428	79.1	313	2	O57596
7	1427.5	79.0	344	2	O93242
8	1357.5	75.2	315	2	O9DGF5
9	1305	72.3	337	2	O6DFY2
10	1305	72.3	337	1	OPCM CHICK
11	1295.5	71.7	338	2	O7Z3W6
12	1276.5	70.7	345	2	O6GM08
13	1276.5	70.6	344	2	O9DF61
14	1270.5	70.3	344	2	O6B014
15	1268	70.2	345	1	OPCM HUMAN
16	1266	70.1	345	1	OPCM BOVIN
17	1259	69.7	345	1	OPCM RAT
18	993.5	55.0	342	2	O642G9
19	946	52.4	334	2	O02870
20	938.5	52.0	338	1	LAMP CHICK
21	931.5	51.6	338	1	LAMP HUMAN
22	930.5	51.5	350	2	O02869
23	926.5	51.3	338	1	LAMP RAT
24	904	50.1	337	2	O6GLZ7
25	894	49.5	341	1	LAMP MOUSE
26	842	46.6	352	2	O9W6V2
27	823	45.6	352	1	NEGR HUMAN
28	815	45.1	348	1	NEGR RAT
29	814	45.1	348	1	NEGR MOUSE
30	759	42.0	325	2	O8HW98
31	686.5	38.0	188	2	O8BMT5

32	656.5	36.4	262	2	O80T70	O80T70 mus musculus
33	599	33.2	261	2	O9W6V1	O9W6V1 gallus gall
34	545.5	30.2	226	2	O8N440	O8N440 homo sapien
35	380.5	21.1	606	2	O9VMN6	O9VMN6 drosophila
36	367	20.3	303	2	O7Q154	O7Q154 anopheles g
37	359.5	19.9	299	2	O7Q863	O7Q863 anopheles g
38	358	19.8	320	2	O7Q0P8	O7Q0P8 anopheles g
39	350.5	19.4	672	2	O8IP70	O8IP70 drosophila
40	349.5	19.4	532	2	O6NNU3	O6NNU3 drosophila
41	349.5	19.4	532	2	O9VLF0	O9VLF0 drosophila
42	348	19.3	554	2	O9W4R3	O9W4R3 drosophila
43	346	19.2	301	2	O7Q864	O7Q864 anopheles g
44	341	18.9	316	2	O7Q0P9	O7Q0P9 anopheles g
45	338.5	18.7	413	2	O9VAR6	O9VAR6 drosophila
46	338	18.7	299	2	O7Q8F3	O7Q8F3 anopheles g
47	333	18.4	315	2	O9VNB2	O9VNB2 drosophila
48	328	18.2	399	2	O7QCH7	O7QCH7 anopheles g
49	318	17.6	340	2	O7Q807	O7Q807 anopheles g
50	313	17.3	550	2	O9VMN9	O9VMN9 drosophila
51	312.5	17.3	285	2	O7PN14	O7PN14 anopheles g
52	308.5	17.1	528	2	P91670	P91670 drosophila
53	306	16.9	545	2	O9VCT4	O9VCT4 drosophila
54	305	16.9	413	2	O7QBV2	O7QBV2 anopheles g
55	303.5	16.8	316	2	O8WPB3	O8WPB3 drosophila
56	300.5	16.6	316	2	O8WP94	O8WP94 drosophila
57	300	16.6	948	2	O9VME2	O9VME2 drosophila
58	299	16.6	401	2	O7PSS8	O7PSS8 anopheles g
59	297.5	16.5	316	2	O8WP58	O8WP58 drosophila
60	297.5	16.5	333	1	AMAL DROME	P15364 drosophila
61	297.5	16.5	341	2	O7K5X2	O7K5X2 drosophila
62	294.5	16.3	383	2	O7QBC5	O7QBC5 anopheles g
63	292.5	16.2	333	2	O7PXA4	O7PXA4 anopheles g
64	290.5	16.1	2673	2	O9GSC3	O9GSC3 homo sapien
65	290.5	16.1	5836	2	O9ERW7	O9ERW7 homo sapien
66	287	15.9	846	2	O57577	O57577 cynops pyrr
67	287	15.9	1100	2	O57576	O57576 cynops pyrr
68	285.5	15.8	413	2	O7QBV1	O7QBV1 anopheles g
69	285.5	15.8	603	2	O9NKF5	O9NKF5 drosophila
70	284	15.7	403	2	O9VPO8	O9VPO8 drosophila
71	283.5	15.7	725	1	NCA2 MOUSE	P13594 mus musculus
72	283.5	15.7	1115	1	NCA1 MOUSE	P13595 mus musculus
73	282.5	15.6	605	2	O921P2	O921P2 mus musculus
74	282.5	15.6	838	2	O8BQ96	O8BQ96 mus musculus
75	282.5	15.6	838	2	O8C4B2	O8C4B2 mus musculus
76	279.5	15.5	725	2	O73633	O73633 xenopus lae
77	279.5	15.5	1091	1	NCA1 CHICK	P13590 gallus gall
78	278.5	15.4	4162	2	O98918	O98918 gallus gall
79	277.5	15.4	719	2	O661V0	O661V0 xenopus lae
80	277.5	15.4	858	1	NCA1 RAT	P13596 rattus norv
81	277.5	15.4	1088	1	NCA1 XENLA	P16170 xenopus lae
82	276.5	15.3	405	2	O6PFK4	O6PFK4 brachydanio
83	276	15.3	761	1	NCA2 HUMAN	P13592 homo sapien
84	276	15.3	848	1	NCA1 HUMAN	P13591 homo sapien
85	275.5	15.3	853	1	NCA1 BOVIN	P11836 bos taurus
86	273.5	15.1	725	2	O73634	O73634 xenopus lae
87	273.5	15.1	433	2	O6DJ83	O6DJ83 xenopus tro
88	272.5	15.1	1323	2	O8476	O8476 gallus gall
89	271.5	15.0	858	2	O86X47	O86X47 homo sapien
90	270.5	15.0	1092	1	NCA2 XENLA	P16335 xenopus lae
91	270	15.0	1479	2	O7KQT5	O7KQT5 drosophila
92	269.5	14.9	484	2	O26475	O26475 schistocerc
93	268.5	14.9	1496	2	O92626	O92626 homo sapien
94	265	14.7	392	2	O7PSN2	O7PSN2 anopheles g
95	265	14.7	1482	2	O9V4Y0	O9V4Y0 drosophila
96	264.5	14.6	1185	2	O7PRK4	O7PRK4 anopheles g
97	263	14.6	1431	2	O80U60	O80U60 mus musculus
98	263	14.6	1431	2	O80U60	O80U60 mus musculus
99	263	14.6	3950	2	O7YRF5	O7YRF5 canis famil
100	261.5	14.5	437	2	O81ZP8	O81ZP8 homo sapien
101	261.5	14.5	1010	1	CONT CHICK	P14781 gallus gall
102	261	14.5	1031	2	O90YM2	O90YM2 brachydanio
103	261	14.5	1395	2	O44924	O44924 drosophila
104	261	14.5	3410	2	O7TN00	O7TN00 rattus norv

105	260.5	14.4	500	2	Q9W260	Q9w260 drosophila	178	229.5	12.7	869	1	MUSK HUMAN	015146 homo sapien
106	260.5	14.4	500	2	Q9X2B7	Q9xzb7 drosophila	179	229	12.7	1056	2	Q90203	Q90z03 xenopus lae
107	260	14.4	601	2	Q96CQ3	Q96cj3 homo sapien	180	229	12.7	4391	1	PGBM HUMAN	P98160 homo sapien
108	260	14.4	1395	2	Q7KVK3	Q7kvk3 drosophila	181	228.5	12.7	1040	1	Q9W675	Q9w675 brachydanio
109	260	14.4	1429	2	Q9W213	Q9w213 drosophila	182	228.5	12.7	1117	2	Q6P1C6	Q6plc6 mus musculus
110	259	14.3	7962	2	Q10465	Q10465 homo sapien	183	228	12.6	1028	2	Q8C6X1	Q8c6x1 mus musculus
111	259	14.3	34350	2	Q8W242	Q8w242 homo sapien	184	227.5	12.6	1051	1	PTK7 CHICK	P91048 gallus gall
112	258.5	14.3	395	2	Q8BXJ7	Q8bxj7 m mus muscu	185	227.5	12.6	1099	2	P97527	P97527 rattus norv
113	258.5	14.3	395	2	Q8BXP4	Q8bxp4 mus musculus	186	227	12.6	1189	2	Q9P2J2	Q9p2j2 homo sapien
114	258.5	14.3	404	2	Q8BLQ9	Q8blq9 mus musculus	187	226.5	12.5	476	2	Q6AYP5	Q6ayp5 rattus norv
115	258.5	14.3	404	2	Q8BYP1	Q8byp1 mus musculus	188	226	12.5	6632	1	UN89 CAEEL	O01761 caenorhabdi
116	257	14.2	1056	2	Q7ZW34	Q7zw34 brachydanio	189	226	12.5	8081	2	Q7Z120	Q7z120 caenorhabdi
117	256	14.2	435	2	Q8N3J6	Q8n3j6 homo sapien	190	225.5	12.5	868	1	MUSK MOUSE	Q61006 mus musculus
118	255.5	14.1	838	2	Q90YMI	Q90ym1 brachydanio	191	225.5	12.5	1388	2	Q7QKD0	Q7qkd0 anopheles g
119	255	14.1	359	1	LACH DROME	Q24372 drosophila	192	225.5	12.4	1662	2	Q7QIV4	Q7qi4 anopheles g
120	255	14.1	359	2	Q9V6C2	Q9v6c2 drosophila	193	224.5	12.4	1224	2	O00533	O00533 homo sapien
121	254.5	14.1	5175	2	Q8I0L3	Q8i0l3 caenorhabdi	194	224	12.4	390	2	Q9H1X9	Q9h1x9 homo sapien
122	254.5	14.1	5198	2	Q765L8	Q765l8 caenorhabdi	195	224	12.4	697	2	Q8NC72	Q8nc72 homo sapien
123	251.5	13.9	837	1	NCM2 MOUSE	Q35136 mus musculus	196	224	12.4	1059	2	Q6UXL7	Q6uxl7 homo sapien
124	250.5	13.9	1342	2	Q9GPP6	Q9gpp6 drosophila	197	224	12.4	1119	2	Q6UXM1	Q6uxm1 homo sapien
125	250.5	13.9	1342	2	Q9VPZ7	Q9vpz7 drosophila	198	224	12.4	1252	2	Q96DN3	Q96dn3 homo sapien
126	250	13.8	349	1	LACH SCHAM	Q26474 schistocerc	199	223	12.3	417	2	Q7TNL1	Q7tnl1 mus musculus
127	250	13.8	525	2	Q7PZ58	Q7pzs8 anopheles g	200	222	12.3	450	2	Q9VR25	Q9vr25 drosophila
128	250	13.8	795	2	Q90YMO	Q90ymo brachydanio	201	222	12.3	595	2	Q6ZRS5	Q6zrs5 homo sapien
129	250	13.8	955	1	MDG1_HUMAN	Q8nf4 homo sapien	202	221.5	12.3	862	1	CD22_MOUSE	F35329 mus musculus
130	249.5	13.6	1040	1	AXO1_HUMAN	Q02246 homo sapien	203	221	12.2	435	2	Q8WR44	Q8wr44 caenorhabdi
131	246.5	13.6	627	2	Q8N466	Q8n466 homo sapien	204	221	12.2	436	2	Q8MPV1	Q8mpv1 caenorhabdi
132	246.5	13.6	727	2	Q6RKB2	Q6rkb2 rattus norv	205	221	12.2	1340	2	Q8NDA2	Q8nda2 homo sapien
133	246.5	13.6	837	2	Q6RKB2	Q6rkb2 rattus norv	206	221	12.2	1746	2	Q8WY19	Q8wy19 homo sapien
134	246.5	13.6	865	2	Q68DA2	Q68da2 homo sapien	207	221	12.2	1827	2	Q9VSG5	Q9vsg5 drosophila
135	246.5	13.6	1018	1	CONT_HUMAN	Q12860 homo sapien	208	221	12.2	2012	1	DSCA_HUMAN	O60469 homo sapien
136	245.5	13.6	1065	1	LIG2_HUMAN	Q94898 homo sapien	209	220.5	12.2	333	2	Q8QWB8	Q8qwb8 homo sapien
137	245	13.6	1028	2	Q6INB5	Q6inb5 xenopus lae	210	220.5	12.2	336	2	Q8OVG4	Q8ovg4 mus musculus
138	244.5	13.5	512	2	Q96DN8	Q96dn8 homo sapien	211	220.5	12.2	336	2	Q9D6E7	Q9d6e7 mus musculus
139	243.5	13.5	837	2	Q7Z7F2	Q7z7f2 homo sapien	212	220.5	12.2	428	2	Q6R3J3	Q6r3j3 mus musculus
140	243.5	13.5	949	1	MDC1_MOUSE	P60755 mus musculus	213	220.5	12.2	443	2	Q8N2F4	Q8n2f4 homo sapien
141	243.5	13.5	956	1	MDC1_HUMAN	Q72553 homo sapien	214	220.5	12.2	445	2	Q8K3T6	Q8k3t6 mus musculus
142	243.5	13.5	1021	1	CONT_RAT	Q63198 rattus norv	215	220.5	12.2	445	2	Q8R4L1	Q8r4l1 mus musculus
143	243.5	13.5	1036	1	AXO1_CHICK	P28685 gallus gall	216	220.5	12.2	456	2	Q8R5M8	Q8r5m8 mus musculus
144	242.5	13.4	949	1	MDC1_RAT	P60756 rattus norv	217	220.5	12.2	898	1	FAS2 SCHAM	P22648 schistocerc
145	242.5	13.4	1020	2	Q6NXY7	Q6nxy7 mus musculus	218	220	12.2	1043	2	Q6PA07	Q6pa07 xenopus lae
146	241.5	13.4	837	1	NCM2_HUMAN	O15394 homo sapien	219	220	12.2	1614	2	Q8UVDT	Q8uvdt xenopus lae
147	241.5	13.4	1018	2	Q28106	Q28106 bos taurus	220	219.5	12.2	330	2	Q90Z42	Q90z42 gallus gall
148	241.5	13.4	1020	1	CONT_MOUSE	P12960 mus musculus	221	219.5	12.2	390	2	Q66KX2	Q66kx2 xenopus lae
149	240.5	13.3	757	2	Q7QCT0	Q7qct0 anopheles g	222	219.5	12.2	442	2	Q9BY67	Q9by67 homo sapien
150	240	13.3	3707	1	PGBM_MOUSE	Q05793 mus musculus	223	219	12.1	1009	2	Q93250	Q93250 xenopus lae
151	237.5	13.2	702	2	Q69ZT8	Q69zv8 mus musculus	224	219	12.1	1026	2	Q8IYW2	Q8iYW2 homo sapien
152	237	13.1	312	2	Q66KV0	Q66kv0 xenopus lae	225	219	12.1	1062	2	Q8BKQ3	Q8bkq3 mus musculus
153	235.5	13.0	632	2	Q6ZRX5	Q6zrx5 homo sapien	226	219	12.1	1091	1	LIG1_MOUSE	P70193 mus musculus
154	235.5	13.0	1027	2	Q90W79	Q90w79 gallus gall	227	219	12.1	1093	1	LIG1_HUMAN	Q96jai homo sapien
155	235.5	13.0	2623	2	Q6WR10	Q6wr10 homo sapien	228	219	12.1	4071	2	Q6KDD1	Q6kdd1 gallus gall
156	234.5	13.0	358	2	Q90490	Q90490 brachydanio	229	218.5	12.1	1114	2	Q9BWV1	Q9bwv1 homo sapien
157	234.5	13.0	779	2	Q97136	Q97136 manduca sex	230	218.5	12.1	1115	2	Q6UXJ5	Q6uxj5 homo sapien
158	234.5	13.0	837	2	Q97137	Q97137 manduca sex	231	218.5	12.1	1612	1	ROB1_MOUSE	Q80936 mus musculus
159	234.5	13.0	1040	1	AXO1_RAT	P22063 rattus norv	232	218	12.1	705	2	Q8CED3	Q8ced3 mus musculus
160	233.5	12.9	1026	2	Q94780	Q94780 homo sapien	233	218	12.1	2013	2	Q8VHZ8	Q8vHz8 rattus norv
161	233.5	12.9	1100	2	Q94779	Q94779 homo sapien	234	218	12.1	2013	2	Q9ERC8	Q9erc8 mus musculus
162	233	12.9	394	2	Q7ZXX1	Q7zxx1 xenopus lae	235	217.5	12.0	348	2	O00557	O00557 homo sapien
163	233	12.9	1028	2	P97528	P97528 rattus norv	236	217.5	12.0	1555	2	Q7PPH8	Q7pph8 anopheles g
164	232.5	12.9	2693	2	Q8ISF3	Q8isf3 caenorhabdi	237	217	12.0	885	2	Q8HYV1	Q8hyv1 sus scrofa
165	232.5	12.9	2708	2	Q8ISF4	Q8isf4 caenorhabdi	238	217	12.0	886	2	Q8HYV2	Q8hyv2 sus scrofa
166	232.5	12.9	18519	2	Q8ISF6	Q8isf6 caenorhabdi	239	217	12.0	1443	2	Q8MTB2	Q8mtb2 drosophila
167	232.5	12.9	18534	2	Q8ISF7	Q8isf7 caenorhabdi	240	217	12.0	1765	2	Q9VS30	Q9vs30 drosophila
168	231.5	12.8	858	2	O18466	O18466 hirudo medi	241	217	12.0	1770	2	Q9VS29	Q9vs29 drosophila
169	231.5	12.8	1005	2	P79921	P79921 xenopus lae	242	216.5	12.0	1109	2	Q6PSH3	Q6psh3 mus musculus
170	231	12.8	703	2	Q21139	Q21139 caenorhabdi	243	215.5	11.9	286	2	Q7PF93	Q7pf93 anopheles g
171	231	12.8	1028	2	Q9U052	Q9u052 homo sapien	244	215.5	11.9	497	2	Q9BXN7	Q9bxn7 homo sapien
172	231	12.8	1028	2	Q9JMB8	Q9jmb8 mus musculus	245	215.5	11.9	714	2	Q6ZPE6	Q6zpe6 mus musculus
173	230.5	12.8	807	2	Q6NY23	Q6ny23 brachydanio	246	215.5	11.9	886	2	Q9VM64	Q9vme4 drosophila
174	230.5	12.8	868	1	MUSK_RAT	Q62838 rattus norv	247	215.5	11.9	1302	1	NRG_DRONE	P20241 drosophila
175	230.5	12.8	1032	2	Q8UVD6	Q8uvd6 brachydanio	248	215.5	11.9	2597	2	Q6WRH9	Q6wrh9 rattus norv
176	230.5	12.8	1040	1	AXO1_MOUSE	Q61330 mus musculus	249	215	11.9	443	2	Q8WR43	Q8wr43 caenorhabdi
177	229.5	12.7	510	2	Q801V8	Q801v8 brachydanio	250	215	11.9	444	2	Q8MPU9	Q8mpu9 caenorhabdi

251 215 11.9 789 2 07PMB2 O7pme2 anopheles g  
 252 215 11.9 1419 2 08SW3 Q8sw3 brachydanio  
 253 214.5 11.9 816 2 08NFA5 Q8nf5 homo sapien  
 254 214.5 11.9 1070 2 06IQ54 Q6iq54 homo sapien  
 255 214.5 11.9 1651 1 ROBI\_RAT Q7rj5 anopheles g  
 256 214 11.8 240 2 07PRJ5 Q7prt5 anopheles g  
 257 214 11.8 498 2 08BRT6 Q8brt6 mus musculus  
 258 213.5 11.8 391 2 07JG1 Q7jg1 anopheles g  
 259 213.5 11.8 398 2 08N126 Q8n126 homo sapien  
 260 213.5 11.8 920 2 08P232 Q8p232 homo sapien  
 261 213.5 11.8 1389 2 090269 Q90269 brachydanio  
 262 213 11.8 484 2 06BEO0 Q6beo0 xenopus lae  
 263 213 11.8 898 2 069226 Q69226 mus musculus  
 264 213 11.8 1134 2 07LBO5 Q7lbo5 brachydanio  
 265 212.5 11.8 1264 2 08P1767 P91767 manduca sex  
 266 212 11.7 1026 2 062845 Q62845 rattus norv  
 267 212 11.7 1151 2 09QVN5 Q9qvn5 rattus sp.  
 268 211.5 11.7 382 2 07PSH7 Q7psh7 anopheles g  
 269 211.5 11.7 749 2 07Q6H1 Q7q6h1 anopheles g  
 270 211.5 11.7 873 1 FAS2\_DROME P34082 drosophila  
 271 211.5 11.7 1070 1 PK77\_HUMAN Q13308 homo sapien  
 272 211.5 11.7 1102 2 0923W7 Q923w7 mus musculus  
 273 211.5 11.7 1109 2 08CE91 Q8ce91 mus musculus  
 274 211.5 11.7 1109 2 06AZB0 Q6azb0 mus musculus  
 275 211.5 11.7 1110 2 08CE73 Q8ce73 mus musculus  
 276 211.5 11.7 1461 1 NEOL\_HUMAN Q92859 homo sapien  
 277 211.5 11.7 1476 2 07QJ29 Q7qj29 anopheles g  
 278 211 11.7 396 2 099N28 Q99n28 m nectin-11  
 279 211 11.7 6620 2 096AA2 Q96aa2 homo sapien  
 280 210 11.6 1561 2 0924D2 Q924d2 mus musculus  
 281 210 11.6 1730 2 07YR07 Q7yrg7 sus scrofa  
 282 210 11.6 1914 1 KMLS\_HUMAN Q15746 homo sapien  
 283 210 11.6 1914 2 07Z4J0 Q7z4j0 homo sapien  
 284 210 11.6 1940 2 06PDN3 Q6pdn3 mus musculus  
 285 209 11.6 504 2 08N441 Q8n441 homo sapien  
 286 209 11.6 504 2 09H4D7 Q9h4d7 homo sapien  
 287 209 11.6 1030 2 08NFA8 Q8nf8 homo sapien  
 288 209 11.6 2222 2 07QEG7 Q7qeg7 anopheles g  
 289 208.5 11.5 1028 2 007409 Q07409 mus musculus  
 290 208.5 11.5 1651 1 ROBI\_HUMAN Q9y6n7 homo sapien  
 291 208 11.5 1155 2 07Q3K8 Q7q3k8 anopheles g  
 292 207.5 11.5 329 2 08N225 Q8n225 homo sapien  
 293 207.5 11.5 1643 2 07QGT8 Q7qgt8 anopheles g  
 294 207 11.5 600 2 08N7W7 Q8n7w7 homo sapien  
 295 206.5 11.4 915 2 08R4B3 Q8r4b3 mus musculus  
 296 206.5 11.4 2016 2 09NBA1 Q9nba1 drosophila  
 297 206 11.4 1187 2 08WR45 Q8wr45 caenorhabdi  
 298 205.5 11.4 1028 2 062682 Q62682 rattus norv  
 299 205.5 11.4 2016 2 08MKM6 Q8mk6 drosophila  
 300 205.5 11.4 2016 2 08MKM7 Q8mk7 drosophila  
 301 205.5 11.4 2019 2 08MKM8 Q8mk8 drosophila  
 302 205.5 11.4 17352 2 095YM2 Q95ym2 procambarus  
 303 205 11.4 432 2 09UJPI Q9ujpi homo sapien  
 304 204.5 11.3 439 2 057349 Q57349 gallus gall  
 305 204.5 11.3 1377 1 NEOL\_RAT P97603 rattus norv  
 306 204.5 11.3 1675 2 0985R4 Q98sw4 brachydanio  
 307 204.5 11.3 3197 2 09WID5 Q9wid5 drosophila  
 308 204 11.3 430 2 07Q6S8 Q7q6s8 anopheles g  
 309 204 11.3 1443 1 NEOL\_CHICK Q90610 gallus gall  
 310 203.5 11.3 1249 2 090Z04 Q90z04 xenopus lae  
 311 203.5 11.3 1316 2 07QE16 Q7qe16 anopheles g  
 312 203.5 11.3 2053 2 08WXU7 Q8wxu7 homo sapien  
 313 203.5 11.3 2092 2 076MU9 Q76mu9 homo sapien  
 314 203.5 11.3 2113 2 08TDB4 Q8td84 homo sapien  
 315 203 11.2 483 2 07SX76 Q7sx76 brachydanio  
 316 203 11.2 1006 2 06IDE9 Q6ide9 drosophila  
 317 203 11.2 1415 2 094155 Q94155 caenorhabdi  
 318 203 11.2 1950 2 080YN8 Q80yn8 mus musculus  
 319 202.5 11.2 496 2 07Z075 Q7z075 caenorhabdi  
 320 202.5 11.2 1066 2 08MSR5 Q8msr5 drosophila  
 321 202.5 11.2 1946 2 068J72 Q68j72 apis mellif  
 322 202.5 11.2 2828 2 09NR99 Q9nr99 homo sapien  
 323 202 11.2 947 1 MUSK\_CHICK Q8axy6 gallus gall

1269 2 001632 O01632 caenorhabdi  
 1273 2 044928 O44928 caenorhabdi  
 1409 2 08J127 Q8j127 brachydanio  
 1409 2 0801M2 Q801m2 brachydanio  
 1428 2 08AY67 Q8ay67 drosophila  
 2022 2 07KQK5 Q7kqk5 drosophila  
 388 2 08NF28 Q8nf28 homo sapien  
 771 2 07QEV8 Q7qev8 anopheles g  
 2008 2 09VEJ5 Q9vej5 drosophila  
 2046 2 07KSE9 Q7kse9 drosophila  
 3215 2 08IRV7 Q8irv7 drosophila  
 3262 2 09EQJ5 Q9eqj5 mus musculus  
 4117 2 08IRV9 Q8irv9 drosophila  
 4179 2 09M4Y4 Q9m4y4 drosophila  
 4223 2 08MPN3 Q8mpn3 drosophila  
 4228 2 08IRV8 Q8irv8 drosophila  
 8647 2 07KQP5 Q7kqp5 drosophila  
 8930 2 07KQP7 Q7kqp7 drosophila  
 8943 2 09V4F7 Q9v4f7 drosophila  
 487 2 07T2H2 Q7t2h2 gallus gall  
 623 2 08BY18 Q8by18 mus musculus  
 688 2 080ZE3 Q80ze3 mus musculus  
 700 1 KIR2\_MOUSE Q07153 torpado cal  
 946 2 07H153 Q07153 torpado cal  
 1709 1 SN\_HUMAN Q9b22 homo sapien  
 1735 2 07Q916 Q7q916 anopheles g  
 1086 2 07QH02 Q7qh02 anopheles g  
 1271 2 06U714 Q6u714 brachydanio  
 1447 1 DCC\_MOUSE P70211 mus musculus  
 1493 1 NEOL\_MOUSE P97798 mus musculus  
 5516 2 07ZZ48 Q7zz48 brachydanio  
 1445 2 063155 Q63155 rattus norv  
 1465 2 07TQG5 Q7tqg5 mus musculus  
 440 2 06ZMD4 Q6zmd4 homo sapien  
 940 2 08NFA7 Q8nfa7 homo sapien  
 1241 1 NPHN\_HUMAN Q60500 homo sapien  
 1513 2 090Z70 Q90z70 brachydanio  
 1723 2 08CHB2 Q8chb2 mus musculus  
 931 2 06KAM5 Q6kam5 mus musculus  
 2053 2 081ZY4 Q81zy4 homo sapien  
 437 2 086YV1 Q86yv1 homo sapien  
 662 2 060926 Q60926 homo sapien  
 847 1 CD22\_HUMAN P20273 homo sapien  
 907 2 09NEG0 Q9neg0 drosophila  
 1240 1 NFAS\_RAT P97685 rattus norv  
 1164 2 066WN5 Q66wn5 drosophila  
 1228 2 08MRA3 Q8mra3 drosophila  
 1235 2 086BD5 Q86bd5 drosophila  
 1235 2 09V787 Q9v787 drosophila  
 1240 1 NFAS\_MOUSE Q810u3 mus musculus  
 1251 2 06ZQ54 Q6zq54 mus musculus  
 1447 1 DCC\_HUMAN P43146 homo sapien  
 16215 2 09NFS3 Q9ntf3 drosophila  
 18074 2 0917U4 Q9i7u4 drosophila  
 537 2 07PSJ8 Q7psj8 anopheles g  
 1240 1 NFAS\_HUMAN Q94856 homo sapien  
 1906 1 KMLS\_CHICK Q9u3p2 caenorhabdi  
 1270 2 09U3P2 Q9u3p2 caenorhabdi  
 1369 1 NFAS\_CHICK Q42414 gallus gall  
 1375 2 08ML47 Q8ml47 drosophila  
 1375 2 094537 Q94537 drosophila  
 1386 1 ROB3\_HUMAN Q96m80 homo sapien  
 1526 2 094538 Q94538 drosophila  
 1526 2 09V6D5 Q9v6d5 drosophila  
 1277 1 CAML\_FUGRU Q98902 fugu rubrip  
 949 2 09VMZ7 Q9vmz7 drosophila  
 1256 1 NRCA\_MOUSE Q810u4 mus musculus  
 749 2 0967D9 Q967d9 drosophila  
 775 2 06PF50 Q6pf50 xenopus lae  
 803 2 08QZP5 Q8qzf5 rattus norv  
 902 2 08IQ17 Q8iq17 drosophila  
 903 2 0967D8 Q967d8 drosophila  
 903 2 09VQY1 Q9vqy1 drosophila



397	193	10.7	949	2	Q8IGN3	Q8ign3 drosophila	470	186	10.3	708	1	KIR2_HUMAN	Q6uw16 homo sapien
398	193	10.7	1166	2	Q9QVNA	Q9qvn4 rattus sp.	471	186	10.3	899	2	Q7PQM9	Q7pqm9 anopheles g
399	193	10.7	1508	2	Q6NR34	Q6nr34 drosophila	472	186	10.3	1325	2	Q6GP61	Q6gp61 xenopus lae
400	193	10.7	1508	2	Q9VOY2	Q9vy2 drosophila	473	186	10.3	2558	2	Q6NR91	Q6nr91 drosophila
401	193	10.7	1531	2	Q967D7	Q967d7 drosophila	474	186	10.3	8648	2	Q7KQP6	Q7kqp6 drosophila
402	193	10.7	2029	1	LAR_DROME	Pl6621 drosophila	475	185.5	10.3	347	2	Q86SN1	Q86sn1 homo sapien
403	193	10.7	2029	2	Q9VIF8	Q9vif8 drosophila	476	185.5	10.3	404	1	RAGE_HUMAN	Q15109 homo sapien
404	192.5	10.7	1150	2	Q8BS24	Q8bs24 mus musculus	477	185.5	10.3	702	1	CEA5_HUMAN	P06731 homo sapien
405	192.5	10.7	1209	2	P70232	P70232 mus musculus	478	185.5	10.3	702	2	Q8N4D0	Q8n4d0 homo sapien
406	192.5	10.7	1259	2	Q6PGJ3	Q6pgj3 mus musculus	479	185.5	10.3	3347	2	Q8MMJ9	Q8mmj9 bombyx mori
407	192.5	10.7	1260	1	CAML_MOUSE	Pl1627 mus musculus	480	185.5	10.3	3354	2	Q8T101	Q8t101 bombyx mori
408	192.5	10.7	1284	1	NRC3A_CHICK	F35331 Gallus gall	481	185	10.2	582	2	Q8R4B5	Q8r4b5 mus musculus
409	192	10.6	399	2	Q8N772	Q8n772 homo sapien	482	185	10.2	778	1	KIR3_MOUSE	Q8br86 mus musculus
410	192	10.6	529	2	Q91V87	Q91v87 mus musculus	483	185	10.2	789	1	KIR1_RAT	Q6x936 rattus norv
411	192	10.6	602	2	Q86YJ9	Q86yj9 homo sapien	484	185	10.2	1020	2	Q8NHN0	Q8nhn0 homo sapien
412	192	10.6	650	2	Q8NA84	Q8na84 homo sapien	485	185	10.2	1020	2	Q8WN20	Q8wn20 homo sapien
413	192	10.6	1256	2	Q35158	Q35158 rattus norv	486	185	10.2	1427	2	Q91562	Q91562 xenopus lae
414	192	10.6	1304	1	NRCA_HUMAN	Q92823 homo sapien	487	184.5	10.2	424	2	Q8C6W0	Q8c6w0 mus musculus
415	192	10.6	1378	1	ROB2_HUMAN	Q9hck4 homo sapien	488	184.5	10.2	570	2	Q6GMZ9	Q6gmz9 xenopus lae
416	191.5	10.6	1060	2	Q9QZT3	Q9qzt3 rattus norv	489	184.5	10.2	826	2	Q7Q1P7	Q7q1p7 anopheles g
417	191	10.6	509	2	Q920C2	Q920c2 mus musculus	490	184.5	10.2	3094	2	Q695L1	Q695l1 homo sapien
418	191	10.6	2154	2	Q8WZ51	Q8wz51 homo sapien	491	184	10.2	421	2	Q7PV30	Q7pv30 anopheles g
419	190.5	10.5	388	2	Q8R464	Q8r464 mus musculus	492	184	10.2	421	2	Q7QLK4	Q7qlk4 anopheles g
420	190.5	10.5	1154	2	Q9QVN3	Q9qvn3 rattus sp.	493	184	10.2	474	2	Q7PKE3	Q7pke3 anopheles g
421	190.5	10.5	1194	2	Q6PW35	Q6pw35 rattus norv	494	184	10.2	626	1	MAG_RAT	F07722 rattus norv
422	190.5	10.5	1197	2	Q6PW38	Q6pw38 rattus norv	495	184	10.2	757	1	KIR1_HUMAN	Q96j84 homo sapien
423	190.5	10.5	1198	2	Q6PW37	Q6pw37 rattus norv	496	184	10.2	1033	2	Q243Z7	Q243z7 drosophila
424	190.5	10.5	1206	2	Q6PW36	Q6pw36 rattus norv	497	184	10.2	1033	2	Q9V643	Q9v643 drosophila
425	190.5	10.5	1209	2	Q6PW39	Q6pw39 rattus norv	498	184	10.2	1302	1	VGR2_BRARE	Q8axb3 brachydanio
426	190.5	10.5	1214	1	NRCA_RAT	P97686 rattus norv	499	183.5	10.2	2213	2	Q7Z5N4	Q7z5n4 homo sapien
427	190.5	10.5	1299	2	Q6PW34	Q6pw34 rattus norv	500	183	10.1	1232	2	Q90284	Q90284 carassius a
428	190.5	10.5	1366	1	ROB3_MOUSE	Q9z214 mus musculus	501	183	10.1	1328	2	Q21043	Q21043 caenorhabdi
429	190.5	10.5	4001	2	Q9N2P7	Q9n2p7 drosophila	502	183	10.1	4816	2	Q8T103	Q8t103 bombyx mori
430	190.5	10.5	4796	2	Q9NL88	Q9nl88 drosophila	503	182.5	10.1	260	2	Q9XXD7	Q9xxd7 caenorhabdi
431	190.5	10.5	4796	2	Q9M055	Q9m055 drosophila	504	182.5	10.1	931	2	Q8NPF26	Q8nfp26 homo sapien
432	190	10.5	345	2	Q811H7	Q811h7 mus musculus	505	182.5	10.1	997	2	Q44087	Q44087 caenorhabdi
433	190	10.5	381	2	Q9Y4A4	Q9y4a4 homo sapien	506	182.5	10.1	1083	2	Q76698	Q76698 caenorhabdi
434	190	10.5	551	2	Q8NHN7	Q8nhn7 homo sapien	507	182.5	10.1	1098	2	Q961D6	Q961d6 drosophila
435	190	10.5	619	2	Q7PX10	Q7pxi0 anopheles g	508	182.5	10.1	1332	2	Q9BN17	Q9bn17 drosophila
436	190	10.5	1406	2	Q9GPP7	Q9gpp7 drosophila	509	182.5	10.1	1332	2	Q9VQW7	Q9vqw7 drosophila
437	190	10.5	1463	2	Q9V044	Q9vq08 drosophila	510	182.5	10.1	1336	1	VGR1_RAT	P53767 rattus norv
438	189.5	10.5	433	2	Q9V644	Q9v644 drosophila	511	182.5	10.1	1944	2	Q695I3	Q695i3 brachydanio
439	189.5	10.5	602	2	Q9VFD9	Q9vfd9 drosophila	512	182	10.1	626	1	MAG_HUMAN	P20916 homo sapien
440	189.5	10.5	765	2	Q9BKQ1	Q9bkq1 aphysia cal	513	182	10.1	877	2	Q9GSH3	Q9gsh3 halocynthia
441	189.5	10.5	765	2	Q9TWA4	Q9twa4 aphysia cal	514	182	10.1	2212	2	Q8NHN3	Q8nhn3 homo sapien
442	189.5	10.5	812	2	Q9BKQ0	Q9bkq0 aphysia cal	515	182	10.1	17903	2	Q7RTL4	Q7rtl4 drosophila
443	189.5	10.5	812	2	Q9TWA5	Q9twa5 aphysia cal	516	181.5	10.0	793	2	Q70246	Q70246 mus musculus
444	189.5	10.5	880	2	Q7KPB8	Q7kpb8 drosophila	517	181.5	10.0	813	2	Q8BQC3	Q8bcq3 mus musculus
445	189.5	10.5	932	2	Q9TKP9	Q9tkp9 aphysia cal	518	181.5	10.0	1125	2	Q7QEC1	Q7qec1 anopheles g
446	189.5	10.5	932	2	Q9TWA6	Q9twa6 aphysia cal	519	181.5	10.0	1197	1	CAML_BRARE	Q90478 brachydanio
447	189.5	10.5	1280	2	Q90933	Q90933 Gallus gall	520	181.5	10.0	1333	1	VGR1_MOUSE	P35969 mus musculus
448	189	10.5	750	2	Q64GH5	Q64gh5 caenorhabdi	521	181	10.0	885	2	Q8N237	Q8n237 homo sapien
449	188.5	10.4	1032	2	Q8AXZ4	Q8axz4 brachydanio	522	181	10.0	913	2	Q8T3E5	Q8t3e5 caenorhabdi
450	188.5	10.4	1036	2	Q8SWW3	Q8sww3 drosophila	523	181	10.0	928	2	Q19128	Q19128 caenorhabdi
451	188.5	10.4	1390	2	Q9VN14	Q9vn14 drosophila	524	181	10.0	955	2	Q8MQ86	Q8mq86 caenorhabdi
452	188.5	10.4	1842	2	Q81ZT3	Q81zt3 homo sapien	525	181	10.0	1244	2	Q69YJ3	Q69yj3 homo sapien
453	188	10.4	529	2	Q7TQM3	Q7tqm3 rattus norv	526	181	10.0	1263	2	Q7Z3B7	Q7z3b7 homo sapien
454	188	10.4	789	1	KIR1_MOUSE	Q80w68 mus musculus	527	181	10.0	3198	2	Q9U8G8	Q9u8g8 manduca sex
455	188	10.4	1177	2	Q6GQB1	Q6gqb1 xenopus lae	528	181	10.0	5604	2	Q8WZ53	Q8wz53 homo sapien
456	187.5	10.4	538	2	Q9QYQ7	Q9qyq7 mus musculus	529	180.5	10.0	848	2	Q25198	Q25198 hydra atten
457	187.5	10.4	1250	2	Q88971	Q88971 mus musculus	530	180.5	10.0	1242	1	NPHN_MOUSE	Q9qza7 mus musculus
458	187.5	10.4	1259	1	CAML_RAT	Q05695 rattus norv	531	180.5	10.0	1256	2	Q925S5	Q925s5 mus musculus
459	187.5	10.4	1266	1	NGCA_CHICK	Q03696 Gallus gall	532	180.5	10.0	1256	2	Q9ET59	Q9et59 mus musculus
460	187.5	10.4	2419	2	Q7PXZ1	Q7pxz1 anopheles g	533	180.5	10.0	1256	2	Q9JIX1	Q9jix1 mus musculus
461	187	10.4	687	2	Q7ZTN4	Q7ztn4 xenopus lae	534	180.5	10.0	1269	2	Q6U7I5	Q6u7i5 brachydanio
462	187	10.4	778	1	KIR3_HUMAN	Q81zu9 homo sapien	535	180	10.0	413	2	Q27418	Q27418 manduca sex
463	187	10.4	1470	1	ROB2_MOUSE	Q7tpd3 mus musculus	536	180	10.0	609	2	Q7QHA0	Q7qha0 anopheles g
464	187	10.4	2133	2	Q7PQG9	Q7pqg9 anopheles g	537	180	10.0	18412	2	Q7Z261	Q7z261 brachydanio
465	187	10.4	2174	2	Q9GQR0	Q9gqr0 drosophila	538	179.5	9.9	333	2	Q90Z41	Q90z41 Gallus gall
466	187	10.4	2995	2	Q696W0	Q696w0 brachydanio	539	179.5	9.9	362	2	Q9JHQ1	Q9jhg1 rattus norv
467	186.5	10.3	922	2	Q90413	Q90413 brachydanio	540	179.5	9.9	503	2	Q9JW259	Q9jw259 drosophila
468	186.5	10.3	1264	2	O14631	O14631 homo sapien	541	179.5	9.9	804	2	Q800Z1	Q800z1 brachydanio
469	186.5	10.3	1889	2	Q7Q0X2	Q7q0x2 anopheles g	542	179.5	9.9	806	2	Q90Z00	Q90z00 brachydanio



689	165.5	9.2	646	1	MU18_HUMAN	P43121	homo sapien	762	160.5	8.9	980	1	KFWS_FELCA	P13369	felis silve
690	165.5	9.2	1023	2	Q9ULI7	Q9UL17	homo sapien	763	160	8.9	319	1	A33_HUMAN	Q99795	homo sapien
691	165.5	9.2	1193	2	Q9VQM1	Q9VQM1	drosofila	764	160	8.9	485	2	Q801W5	Q801W5	brachydanio
692	165	9.1	584	2	Q9Y3Y8	Q9Y3Y8	homo sapien	765	160	8.9	544	2	Q7Z285	Q7Z285	brachydanio
693	165	9.1	822	1	FGRI_MOUSE	P16032	mus musculus	766	160	8.9	564	1	C166_BRARE	Q90460	brachydanio
694	165	9.1	822	1	FGRI_MOUSE	Q04589	rattus norv	767	160	8.9	564	1	C166_BRARE	Q61QX4	brachydanio
695	165	9.1	822	2	Q60818	Q60818	mus musculus	768	160	8.9	640	2	Q8BSM2	Q8BSM2	mus musculus
696	165	9.1	998	2	Q9W4Y6	Q9W4Y6	drosofila	769	160	8.9	822	1	FGRI_MOUSE	Q11362	homo sapien
697	165	9.1	1014	2	Q8NFA6	Q8NFA6	homo sapien	770	160	8.9	1144	2	Q18100	Q18100	caenorhabdi
698	165	9.1	2222	2	Q97394	Q97394	drosofila	771	160	8.9	1437	2	Q44329	Q44329	hirudo medi
699	165	9.1	2230	2	Q86B07	Q86B07	drosofila	772	160	8.9	6839	2	Q23550	Q23550	caenorhabdi
700	164.5	9.1	438	2	Q920C3	Q920C3	mus musculus	773	159.5	8.8	570	2	Q8NCE6	Q8NCE6	homo sapien
701	164.5	9.1	583	1	C166_HUMAN	Q13740	homo sapien	774	159.5	8.8	585	2	Q6UY09	Q6UY09	homo sapien
702	164.5	9.1	583	1	C166_HUMAN	Q31112	rattus norv	775	159.5	8.8	975	2	Q97174	Q97174	drosofila
703	164.5	9.1	639	2	Q96P30	Q96P30	homo sapien	776	159	8.8	226	2	Q7PUJ2	Q7PUJ2	anopheles g
704	164.5	9.1	822	2	Q61674	Q61674	drosofila	777	159	8.8	816	2	Q91285	Q91285	pleurodeles
705	164.5	9.1	822	2	Q9V6T1	Q9V6T1	drosofila	778	159	8.8	1948	1	PTNS_HUMAN	Q13332	homo sapien
706	164.5	9.1	1247	2	Q7Q0S6	Q7Q0S6	anopheles g	779	158.5	8.8	388	1	BASI_CHICK	P17790	gallus gall
707	164	9.1	310	2	Q68FQ2	Q68FQ2	rattus norv	780	158.5	8.8	912	1	ICAS_RABIT	Q28730	oryctolagus
708	164	9.1	310	2	Q9DLM9	Q9DLM9	mus musculus	781	158.5	8.8	1199	2	Q21041	Q21041	caenorhabdi
709	164	9.1	310	2	Q9D8B7	Q9D8B7	mus musculus	782	158.5	8.8	1215	2	Q7KTI7	Q7KTI7	drosofila
710	164	9.1	310	2	Q9EPK4	Q9EPK4	m junctiona	783	158.5	8.8	1461	2	Q8T9F6	Q8T9F6	drosofila
711	164	9.1	628	1	LU_HUMAN	P50895	homo sapien	784	158.5	8.8	1474	2	Q8T4M0	Q8T4M0	drosofila
712	164	9.1	628	2	Q86VC7	Q86VC7	homo sapien	785	158.5	8.8	1503	2	Q7KTI8	Q7KTI8	drosofila
713	164	9.1	812	2	Q8N612	Q8N612	homo sapien	786	158.5	8.8	1509	2	Q81PG1	Q81PG1	drosofila
714	164	9.1	820	2	Q8C1M9	Q8C1M9	mus musculus	787	158.5	8.8	1509	2	Q81PG1	Q81PG1	drosofila
715	164	9.1	924	2	Q8TAM9	Q8TAM9	homo sapien	788	158	8.7	242	2	Q7Q1Q0	Q7Q1Q0	anopheles g
716	164	9.1	998	2	Q9SR27	Q9SR27	drosofila	789	158	8.7	293	2	Q7QC80	Q7QC80	anopheles g
717	164	9.1	1311	2	Q961K8	Q961K8	drosofila	790	158	8.7	360	2	Q61565	Q61565	mus musculus
718	164	9.1	1994	2	Q6ZPP2	Q6ZPP2	mus musculus	791	158	8.7	361	2	Q9QM79	Q9QM79	mus sp. . . f
719	164	9.1	2176	2	Q6V4S5	Q6V4S5	mus musculus	792	158	8.7	697	2	Q7PMJ7	Q7PMJ7	anopheles g
720	163.5	9.1	483	2	Q9DBP8	Q9DBP8	mus musculus	793	158	8.7	822	2	Q9QVW7	Q9QVW7	rattus sp.
721	163.5	9.1	508	2	Q8CED8	Q8CED8	mus musculus	794	157.5	8.7	346	2	Q9CTL3	Q9CTL3	mus musculus
722	163.5	9.1	508	2	Q8R007	Q8R007	mus musculus	795	157.5	8.7	441	2	Q8C139	Q8C139	mus musculus
723	163.5	9.1	513	2	Q9D6N4	Q9D6N4	mus musculus	796	157.5	8.7	496	2	Q9JIF9	Q9JIF9	mus musculus
724	163.5	9.1	646	2	Q6PHR3	Q6PHR3	homo sapien	797	157.5	8.7	531	2	Q7QEV7	Q7QEV7	anopheles g
725	163.5	9.1	1596	2	Q9HCL6	Q9HCL6	homo sapien	798	157.5	8.7	583	1	C166_MOUSE	Q61490	mus musculus
726	163	9.0	357	2	Q18872	Q18872	sus scrofa	799	157.5	8.7	697	1	SILA_HUMAN	Q961C7	homo sapien
727	163	9.0	324	1	ICAS_HUMAN	Q9UMF0	homo sapien	800	157.5	8.7	939	2	Q9VB35	Q9VB35	drosofila
728	162.5	9.0	332	2	Q684Q2	Q684Q2	mus musculus	801	157.5	8.7	939	2	Q9VB35	Q9VB35	drosofila
729	162.5	9.0	353	2	Q86XY3	Q86XY3	homo sapien	802	157.5	8.7	978	1	KFWS_FSVMD	P00545	feline sarc
730	162.5	9.0	508	2	Q96LA5	Q96LA5	homo sapien	803	157.5	8.7	1052	2	Q7PMY4	Q7PMY4	anopheles g
731	162.5	9.0	605	2	Q6GNL9	Q6GNL9	xenopus lae	804	157.5	8.7	1503	2	Q8T4L8	Q8T4L8	drosofila
732	162.5	9.0	628	2	Q9MZ08	Q9MZ08	bos taurus	805	157	8.7	298	1	JAMI_BOVIN	Q9X556	bos taurus
733	162.5	9.0	1509	2	Q95PI0	Q95PI0	drosofila	806	157	8.7	299	1	JAMI_HUMAN	Q9Y624	homo sapien
734	162.5	9.0	1535	2	Q23991	Q23991	drosofila	807	157	8.7	383	2	Q75ML9	Q75ML9	homo sapien
735	162	9.0	773	2	Q7QBL9	Q7QBL9	anopheles g	808	157	8.7	446	2	Q63236	Q63236	rattus norv
736	162	9.0	1304	2	Q9VBE5	Q9VBE5	drosofila	809	157	8.7	641	2	Q86SD2	Q86SD2	ciona intes
737	162	9.0	4824	2	Q95YM1	Q95YM1	procamburus	810	157	8.7	734	2	Q96LA4	Q96LA4	homo sapien
738	161.5	8.9	350	2	Q9VFU7	Q9VFU7	drosofila	811	157	8.7	734	2	Q96P31	Q96P31	homo sapien
739	161.5	8.9	402	2	Q9NAR0	Q9NAR0	caenorhabdi	812	157	8.7	742	2	Q8N6S2	Q8N6S2	homo sapien
740	161.5	8.9	638	2	Q7Q766	Q7Q766	anopheles g	813	156.5	8.7	416	1	RAGE_BOVIN	Q28173	bos taurus
741	161.5	8.9	650	2	Q9GKR2	Q9GKR2	bos taurus	814	156.5	8.7	799	2	Q8C3V5	Q8C3V5	mus musculus
742	161.5	8.9	739	2	Q9GKR3	Q9GKR3	bos taurus	815	156.5	8.7	799	2	Q8CIB8	Q8CIB8	mus musculus
743	161.5	8.9	802	2	Q42127	Q42127	xenopus lae	816	156.5	8.7	811	2	Q9YH43	Q9YH43	xenopus lae
744	161.5	8.9	2325	2	Q9N3X8	Q9N3X8	caenorhabdi	817	156	8.6	525	2	Q7QJK5	Q7QJK5	anopheles g
745	161.5	8.9	2935	2	Q7Z1Y4	Q7Z1Y4	drosofila	818	156	8.6	692	2	Q800Y9	Q800Y9	brachydanio
746	161.5	8.9	2946	2	Q9W053	Q9W053	drosofila	819	156	8.6	740	2	Q800P29	Q800P29	homo sapien
747	161	8.9	298	2	Q8INK5	Q8INK5	drosofila	820	156	8.6	756	2	Q800Z0	Q800Z0	brachydanio
748	161	8.9	309	2	Q96FL1	Q96FL1	homo sapien	821	156	8.6	977	1	KFMS_MOUSE	P09581	mus musculus
749	161	8.9	310	1	JAM3_HUMAN	Q9BX67	homo sapien	822	156	8.6	978	1	KFMS_MOUSE	Q00495	rattus norv
750	161	8.9	336	2	Q96IT8	Q96IT8	drosofila	823	156	8.6	1501	2	Q7KUK9	Q7KUK9	drosofila
751	161	8.9	461	2	Q13854	Q13854	homo sapien	824	156	8.6	1860	2	Q7PQF4	Q7PQF4	anopheles g
752	161	8.9	527	2	Q6ZTR2	Q6ZTR2	homo sapien	825	156	8.6	7158	2	Q23551	Q23551	caenorhabdi
753	161	8.9	538	2	Q29123	Q29123	sus scrofa	826	155.5	8.6	761	2	Q951Q2	Q951Q2	macaca fasc
754	161	8.9	605	2	Q8TBU0	Q8TBU0	homo sapien	827	155.5	8.6	880	1	TYO3_MOUSE	P55144	mus musculus
755	161	8.9	693	2	Q9UPU1	Q9UPU1	homo sapien	828	155.5	8.6	880	2	Q6NZM6	Q6NZM6	mus musculus
756	161	8.9	1327	2	Q8QHL3	Q8QHL3	gallus gall	829	155	8.6	373	2	Q9HEB4	Q9HEB4	homo sapien
757	161	8.9	1345	2	Q8VCD0	Q8VCD0	mus musculus	830	155	8.6	454	2	Q91W54	Q91W54	mus musculus
758	161	8.9	2541	2	Q19663	Q19663	caenorhabdi	831	155	8.6	458	2	Q61351	Q61351	mus musculus
759	160.5	8.9	422	2	Q86CY9	Q86CY9	helicoverpa	832	155	8.6	521	1	CEA1_MOUSE	P31809	mus musculus
760	160.5	8.9	646	2	Q95812	Q95812	homo sapien	833	155	8.6	521	2	Q925P3	Q925P3	mus musculus
761	160.5	8.9	646	2	Q8NHN8	Q8NHN8	homo sapien	834	155	8.6	521	2	Q61352	Q61352	mus musculus

835 155 8.6 707 2 Q7PMWJ1 Q7pwj1 anopheles g  
836 155 8.6 819 1 FGR1 CHICK P21804 gallus gall  
837 155 8.6 977 1 Q6R09 Q6frd9 homo sapien  
838 155 8.6 1363 1 VGR3 MOUSE P35918 mus musculus  
839 155 8.6 1367 1 VGR2 MOUSE P35918 mus musculus  
840 154.5 8.6 602 1 NRG1 CHICK Q05199 gallus gall  
841 154.5 8.6 1897 1 PTFP HUMAN P10586 homo sapien  
842 154.5 8.6 1898 1 Q6W50 Q6w60 homo sapien  
843 154 8.5 549 2 QSD006 Q8d006 mus musculus  
844 154 8.5 606 2 Q8ESS7 Q8ess7 mus musculus  
845 154 8.5 624 2 Q8ESS6 Q8ess6 rattus norv  
846 154 8.5 648 2 Q8EPF1 Q8epf1 mus musculus  
847 154 8.5 648 2 Q8R2Y2 Q8r2y2 mus musculus  
848 154 8.5 686 1 IPL2 HUMAN Q9np60 h x-linked  
849 154 8.5 816 2 Q86PM4 Q86pm4 hydra atten  
850 154 8.5 1348 1 VGR2 COTJA P32583 coturnix co  
851 153.5 8.5 280 2 Q3350 Q93350 caenorhabdi  
852 153.5 8.5 1173 2 Q6NR54 Q6nr54 drosophila  
853 153.5 8.5 2217 2 Q8AV57 Q8av57 gallus gall  
854 153.5 8.5 6048 2 Q7JN85 Q7jn85 caenorhabdi  
855 153 8.5 307 2 Q7PCU3 Q7pcu3 anopheles g  
856 153 8.5 1348 2 Q87WM1 Q87wm1 gallus gall  
857 153 8.5 1788 2 Q9IAJ0 Q9iaj0 xenopus lae  
858 152.5 8.4 347 1 PRPD HUMAN P23468 homo sapien  
859 152.5 8.4 347 2 Q6PJ52 Q6pjs2 homo sapien  
860 152.5 8.4 509 2 Q9EQV5 Q9eqv5 m mman-g pr  
861 152.5 8.4 519 1 ECTO RAT Q9eqv5 rattus norv  
862 152.5 8.4 1802 2 Q28633 Q28633 oryctolagus  
863 152.5 8.4 7105 2 Q7PXMW9 Q7pxmw9 anopheles g  
864 152 8.4 247 2 Q7PVM3 Q7pvm3 anopheles g  
865 152 8.4 636 2 Q22040 Q22040 caenorhabdi  
866 152 8.4 687 2 Q9JJ08 Q9jj08 rattus norv  
867 152 8.4 783 2 Q86T42 Q86t42 homo sapien  
868 152 8.4 810 2 Q7PUH1 Q7puh1 anopheles g  
869 152 8.4 880 1 TYO3 RAT P55146 rattus norv  
870 152 8.4 1024 2 Q63HJ3 Q63hj3 homo sapien  
871 152 8.4 1092 2 Q91ZT0 Q91zt0 rattus norv  
872 152 8.4 1141 1 MYPS HUMAN Q00872 homo sapien  
873 152 8.4 1148 2 Q8N3I2 Q8n3i2 homo sapien  
874 152 8.4 1148 2 Q8N3R4 Q8n3r4 homo sapien  
875 152 8.4 1148 2 Q86T39 Q86t39 homo sapien  
876 152 8.4 1171 2 Q86T48 Q86t48 homo sapien  
877 152 8.4 1171 2 Q86T08 Q86tc8 homo sapien  
878 152 8.4 1343 1 VGR2 RAT Q08775 rattus norv  
879 152 8.4 1363 2 Q91ZT1 Q91zt1 rattus norv  
880 151.5 8.4 228 2 Q7PVM5 Q7pvm5 anopheles g  
881 151.5 8.4 229 2 Q7PUC4 Q7puc4 anopheles g  
882 151.5 8.4 344 1 CEAG HUMAN P40199 homo sapien  
883 151.5 8.4 344 2 Q13774 Q13774 homo sapien  
884 151.5 8.4 564 2 Q7ZU00 Q7zu00 brachydanio  
885 151.5 8.4 847 2 Q8BFR2 Q8bf2 m mus muscu  
886 151.5 8.4 847 2 Q8C4T3 Q8c4t3 mus musculus  
887 151.5 8.4 948 2 Q9TDT7 Q9tdt7 trichosurus  
888 151.5 8.4 1898 2 Q9EQI7 Q9eqi7 mus musculus  
889 151 8.4 413 2 Q699P0 Q699p0 antheraea p  
890 151 8.4 1156 2 Q676C3 Q676c3 oikopleura  
891 150.5 8.3 422 2 Q7RTV9 Q7rtv9 homo sapien  
892 150.5 8.3 437 2 Q8NFS6 Q8nf56 homo sapien  
893 150.5 8.3 509 2 Q91YK7 Q91yk7 mus musculus  
894 150.5 8.3 510 2 Q96K15 Q96k15 homo sapien  
895 150.5 8.3 510 2 Q96KN15 Q96kn15 homo sapien  
896 150.5 8.3 824 2 Q90749 Q90749 gallus gall  
897 150.5 8.3 888 2 Q7ZWM9 Q7zwm9 xenopus lae  
898 150.5 8.3 961 1 ROB4 RAT Q80W87 rattus norv  
899 150.5 8.3 1298 1 VGR3 HUMAN P35916 homo sapien  
900 150.5 8.3 1298 2 Q86W08 Q86w08 homo sapien  
901 150.5 8.3 1363 2 Q86W07 Q86w07 homo sapien  
902 150 8.3 343 2 Q7TP22 Q7tp22 rattus norv  
903 150 8.3 685 1 IPL2 MOUSE Q9er56 mus musculus  
904 150 8.3 711 2 Q24205 Q24205 drosophila  
905 150 8.3 977 2 Q6NXV8 Q6nxv8 mus musculus  
906 150 8.3 1171 2 Q86T48 Q86t48 homo sapien  
907 149.5 8.3 349 1 CEAG\_HUMAN P31997 homo sapien

908 149.5 8.3 360 2 Q8BJ10 Q8bj10 mus musculus  
909 149.5 8.3 739 1 VCAL RAT P29534 rattus norv  
910 149.5 8.3 815 2 Q80SB9 Q80sb9 brachydanio  
911 149.5 8.3 1073 2 Q9WIR8 Q9wit8 drosophila  
912 149.5 8.3 1250 2 Q8TDY8 Q8tdy8 homo sapien  
913 149.5 8.3 1501 2 Q9QW00 Q9qw00 rattus sp.  
914 149.5 8.3 1863 2 Q64605 Q64605 rattus norv  
915 149 8.3 335 2 Q75237 Q75237 homo sapien  
916 149 8.3 372 2 Q8KIG0 Q8ki90 rattus norv  
917 149 8.3 373 2 Q8R373 Q8r373 mus musculus  
918 149 8.3 388 2 Q9Z151 Q9z151 mus musculus  
919 149 8.3 570 2 Q6GLY1 Q6glly1 xenopus lae  
920 149 8.3 1894 2 Q64487 Q64487 mus musculus  
921 148.5 8.2 220 2 Q7PX67 Q7px67 anopheles g  
922 148.5 8.2 289 2 Q7ZWT0 Q7zwt0 xenopus lae  
923 148.5 8.2 476 2 Q7ZXJ8 Q7zxj8 xenopus lae  
924 148.5 8.2 521 1 C166 CANFA Q46634 canis famil  
925 148.5 8.2 536 2 Q9GV82 Q9gv82 drosophila  
926 148.5 8.2 588 1 C166 CHICK P42292 gallus gall  
927 148.5 8.2 673 2 Q6M2W2 Q6m2w2 homo sapien  
928 148.5 8.2 821 2 Q9YH44 Q9yh44 xenopus lae  
929 148.5 8.2 1173 2 Q9V7J8 Q9v7j8 drosophila  
930 148.5 8.2 1501 2 Q7TT17 Q7tt17 mus musculus  
931 148.5 8.2 1502 2 Q9UM81 Q9um81 homo sapien  
932 148.5 8.2 1887 2 Q9QW67 Q9qw67 rattus sp.  
933 148.5 8.2 1904 2 Q64699 Q64699 mus musculus  
934 148 8.2 622 2 Q9JXB2 Q9jkb2 mus musculus  
935 148 8.2 694 2 Q8SWT7 Q8swt7 drosophila  
936 148 8.2 697 2 Q8TC35 Q8tc35 homo sapien  
937 148 8.2 709 2 Q8IXC7 Q8ixc7 homo sapien  
938 147.5 8.2 229 2 Q7PVL3 Q7pvl3 anopheles g  
939 147.5 8.2 318 2 Q91664 Q91664 xenopus lae  
940 147.5 8.2 331 2 Q63239 Q63239 rattus norv  
941 147.5 8.2 403 1 RAGE\_MOUSE Q62151 mus musculus  
942 147.5 8.2 446 2 Q63237 Q63237 rattus norv  
943 147.5 8.2 573 2 Q6GN50 Q6gn50 xenopus lae  
944 147.5 8.2 876 2 Q78E87 Q78e87 mus musculus  
945 147.5 8.2 1499 2 Q90815 Q90815 gallus gall  
946 147 8.1 402 2 Q35444 Q35444 mus musculus  
947 147 8.1 549 2 Q9NQ53 Q9nq53 homo sapien  
948 147 8.1 739 1 PECI\_BOVIN P51866 bos taurus  
949 147 8.1 1044 2 Q961W3 Q961w3 homo sapien  
950 147 8.1 1237 2 Q75147 Q75147 homo sapien  
951 147 8.1 1252 2 Q9JLI1 Q9jli1 mus musculus  
952 146.5 8.1 275 2 Q7PVM4 Q7pvm4 anopheles g  
953 146.5 8.1 291 2 Q658Q7 Q658q7 homo sapien  
954 146.5 8.1 326 2 Q8NC17 Q8nc17 homo sapien  
955 146.5 8.1 468 2 Q9XY08 Q9xy08 bombyx mori  
956 146.5 8.1 484 2 Q99JQ8 Q99jq8 mus musculus  
957 146.5 8.1 606 2 Q9ESS8 Q9es88 rattus norv  
958 146.5 8.1 648 2 Q9EPF2 Q9epf2 rattus norv  
959 146.5 8.1 773 2 Q9NSW7 Q9nsw7 homo sapien  
960 146.5 8.1 847 2 Q8N475 Q8n475 homo sapien  
961 146.5 8.1 850 2 Q9ULF7 Q9ulf7 homo sapien  
962 146.5 8.1 1280 2 Q9EPX2 Q9epx2 mus musculus  
963 146 8.1 309 2 Q7QFT7 Q7qft7 anopheles g  
964 146 8.1 486 2 Q8CGH8 Q8cgh8 mus musculus  
965 146 8.1 549 2 Q9JLB9 Q9jlb9 mus musculus  
966 146 8.1 738 2 P79390 P79390 bos primige  
967 146 8.1 782 2 Q61563 Q61563 mus musculus  
968 146 8.1 790 2 Q8C4N3 Q8c4n3 mus musculus  
969 146 8.1 827 1 TRKC CHICK Q91044 gallus gall  
970 146 8.1 1087 2 Q7ZY71 Q7zy71 xenopus lae  
971 146 8.1 1088 1 PGDS\_RAT P20786 rattus norv  
972 146 8.1 1089 1 PGDS\_MOUSE P26618 mus musculus  
973 146 8.1 1089 2 Q7TSJ3 Q7tsj3 mus musculus  
974 145.5 8.1 292 2 Q6GI72 Q6gi72 brachydanio  
975 145.5 8.1 504 2 Q6NNA1 Q6nna1 drosophila  
976 145.5 8.1 508 2 Q9VGD2 Q9vgd2 drosophila  
977 145.5 8.1 520 2 Q925P2 Q925p2 mus musculus  
978 145.5 8.1 664 2 Q9VGD3 Q9vgd3 drosophila  
979 145.5 8.1 739 1 VCAL\_MOUSE P29533 mus musculus  
980 145.5 8.1 739 2 Q91X98 Q91x98 mus musculus

981	145.5	8.1	808	1	FGR4_MOUSE	Q03142 mus musculus
982	145.5	8.1	831	2	Q71S19	Q71S19 gallus gall
983	145.5	8.1	1012	1	ROB4_MOUSE	Q8C310 mus musculus
984	145.5	8.1	1898	2	Q64604	Q64604 r protein-t
985	145	8.0	259	2	Q9Y5B2	Q9Y5B2 homo sapien
986	145	8.0	373	2	Q920S5	Q920S5 mus musculus
987	145	8.0	622	2	Q9ES55	Q9ES55 mus musculus
988	145	8.0	782	2	Q9TT23	Q9TT23 oryctolagus
989	145	8.0	812	2	Q8MZ57	Q8MZ57 drosophila
990	145	8.0	878	2	Q8GV22	Q8GV22 mytilus gal
991	145	8.0	972	1	KFMS_HUMAN	P07333 homo sapien
992	145	8.0	972	2	Q86VW7	Q86VW7 homo sapien
993	145	8.0	1450	2	Q7QC22	Q7QC22 anopheles g
994	144.5	8.0	203	2	Q7PVM1	Q7PVM1 anopheles g
995	144.5	8.0	421	2	Q9NBB2	Q9NBB2 drosophila
996	144.5	8.0	606	2	Q61RH8	Q61RH8 rattus norv
997	144.5	8.0	739	2	Q8K0X1	Q8K0X1 mus musculus
998	144.5	8.0	754	2	Q8BZ76	Q8BZ76 m mus muscu
999	144.5	8.0	880	2	Q8QFP9	Q8QFP9 xenopus lae
1000	144	8.0	260	2	Q7FZ33	Q7FZ33 anopheles g
1001	144	8.0	278	2	Q9XYL3	Q9XYL3 mus musculus
1002	144	8.0	413	2	Q6ZNI1	Q6ZNI1 homo sapien
1003	144	8.0	422	2	Q8WR61	Q8WR61 lymantria d
1004	144	8.0	434	2	Q6DN72	Q6DN72 homo sapien
1005	144	8.0	438	2	Q9JLB7	Q9JLB7 mus musculus
1006	144	8.0	510	2	Q9JLB8	Q9JLB8 mus musculus
1007	144	8.0	542	2	Q8NHNS	Q8NHNS homo sapien
1008	144	8.0	891	2	Q25177	Q25177 hydra atten
1009	143.5	7.9	296	2	Q640C0	Q640C0 xenopus lae
1010	143.5	7.9	300	2	Q7SYQ7	Q7SYQ7 xenopus lae
1011	143.5	7.9	430	2	Q8N4F1	Q8N4F1 homo sapien
1012	143.5	7.9	1177	2	Q21391	Q21391 caenorhabdi
1013	143.5	7.9	12268	2	Q8MQ08	Q8MQ08 caenorhabdi
1014	143.5	7.9	13100	2	Q09165	Q09165 caenorhabdi
1015	143	7.9	442	2	Q8C306	Q8C306 mus musculus
1016	143	7.9	620	1	SMP_COTUA	Q92154 coturnix co
1017	143	7.9	688	2	Q55095	Q55095 mus musculus
1018	143	7.9	688	2	Q8K1H4	Q8K1H4 mus musculus
1019	143	7.9	814	2	Q9VNP2	Q9VNP2 drosophila
1020	143	7.9	972	2	Q76110	Q76110 callithrix
1021	143	7.9	977	2	Q9I8N6	Q9I8N6 brachydanio
1022	143	7.9	1011	2	Q24273	Q24273 drosophila
1023	143	7.9	1383	2	Q7Q840	Q7Q840 anopheles g
1024	142.5	7.9	324	2	Q8NBY8	Q8NBY8 homo sapien
1025	142.5	7.9	326	2	Q9UPX8	Q9UPX8 homo sapien
1026	142.5	7.9	435	1	PSG6_HUMAN	Q00889 homo sapien
1027	142.5	7.9	515	2	Q96R50	Q96R50 homo sapien
1028	142.5	7.9	715	2	Q9NKA6	Q9NKA6 drosophila
1029	142.5	7.9	739	1	VCAL_HUMAN	P19320 homo sapien
1030	142.5	7.9	956	1	UNSD_MOUSE	Q8K182 mus musculus
1031	142.5	7.9	1019	2	Q8UVR8	Q8UVR8 fugu rubrip
1032	142.5	7.9	1052	2	Q9VUC8	Q9VUC8 drosophila
1033	142	7.9	344	2	Q8WR42	Q8WR42 caenorhabdi
1034	142	7.9	345	2	Q8MPV0	Q8MPV0 caenorhabdi
1035	142	7.9	494	2	Q9ESC6	Q9ESC6 mus musculus
1036	142	7.9	505	2	Q9U965	Q9U965 geodia cydo
1037	142	7.9	806	1	CEK2_CHICK	P18460 gallus gall
1038	142	7.9	1252	2	Q9EQS9	Q9EQS9 mus musculus
1039	142	7.9	1253	2	Q9EQS8	Q9EQS8 mus musculus
1040	141.5	7.8	324	2	Q9UPK9	Q9UPK9 homo sapien
1041	141.5	7.8	333	2	Q75238	Q75238 homo sapien
1042	141.5	7.8	881	2	Q965M2	Q965M2 caenorhabdi
1043	141.5	7.8	953	1	UNSD_HUMAN	Q8UX24 homo sapien
1044	141.5	7.8	1007	1	ROB4_HUMAN	Q8UX25 homo sapien
1045	141.5	7.8	1227	2	Q21038	Q21038 caenorhabdi
1046	141.5	7.8	1447	2	Q16779	Q16779 caenorhabdi
1047	141.5	7.8	2000	2	Q97791	Q97791 oryctolagus
1048	141	7.8	276	2	Q6P0R7	Q6P0R7 brachydanio
1049	141	7.8	338	2	Q6DHD4	Q6DHD4 brachydanio
1050	141	7.8	432	2	Q6DDE7	Q6DDE7 xenopus lae
1051	141	7.8	456	2	Q7PUM9	Q7PUM9 anopheles g
1052	141	7.8	626	2	Q6DCH3	Q6DCH3 xenopus lae
1053	141	7.8	815	2	Q8AYP3	Q8AYP3 brachydanio

P21802	homo sapien
Q8VI99	rattus norv
Q8VIA0	rattus norv
Q98SU1	danio nigro
Q63710	rattus ratt
Q965M3	caenorhabdi
Q6P4H5	homo sapien
Q90699	gallus gall
P18461	gallus gall
Q6E7G6	canis famil
P16234	homo sapien
Q9IAI9	gallus gall
Q6YNR7	brachydanio
Q9R069	mus musculus
Q99K86	mus musculus
Q7QJK6	anopheles g
Q9XY54	hydra atten
Q99052	mus musculus
Q7TSI8	mus musculus
Q918X3	brachydanio
Q61851	mus musculus
Q9P2B2	homo sapien
Q06418	homo sapien
Q86VR3	homo sapien
Q99662	homo sapien
F10721	homo sapien
Q6IQ28	homo sapien
Q7QC00	anopheles g
Q8MMK1	bombyx mori
Q9TXK2	caenorhabdi
Q8MXD7	caenorhabdi
Q8MXD8	caenorhabdi
Q9TXK2	caenorhabdi
P11464	homo sapien
Q96P33	homo sapien
Q96P35	homo sapien
Q7ZY97	xenopus lae
Q7ZZ47	brachydanio
Q28260	canis famil
Q6PLM7	homo sapien
P21803	mus musculus
Q9147	drosophila
Q676A1	oikopleura
Q6NZV3	brachydanio
Q93360	hyphantria
Q95YM9	halocynthia
Q91286	pleurodeles
Q9W755	brachydanio
Q8UW13	lapemis har
Q8N732	homo sapien
Q9VQY0	drosophila
Q26438	hyalophora
Q96QL5	homo sapien
Q9U4G1	drosophila
Q9IAJ1	xenopus lae
Q9U964	geodia cydo
Q9GL76	sus scrofa
Q86YC7	homo sapien
P26619	xenopus lae
Q63238	rattus norv
Q9VKX8	drosophila
P25033	hyalophora
Q00888	homo sapien
Q9BRW2	homo sapien
Q66J72	xenopus lae
Q95242	sus scrofa
Q98U41	danio abol
Q8NNH2	homo sapien
P79701	coturnix co
Q6NVZ3	homo sapien
Q68DM9	homo sapien

1127	137	7.6	424	1	PSGA_HUMAN	Q15235	homo sapien	1200	133.5	7.4	888	1	UFO_MOUSE	Q00993	mus musculus
1128	137	7.6	448	2	OBIGAS	Q8iga5	drosophila	1201	133.5	7.4	888	2	Q80YQ3	Q80YQ3	mus musculus
1129	137	7.6	448	2	QJHL7	Q8jhl7	rattus norv	1202	133.5	7.4	959	2	Q6PUN9	Q6PUN9	amysoma m
1130	137	7.6	458	2	Q63093	Q63093	rattus norv	1203	133.5	7.4	1598	2	Q9P214	Q9P214	homo sapien
1131	137	7.6	459	2	Q63093	Q63093	rattus norv	1204	133	7.4	317	2	Q9ESA2	Q9esa2	rattus norv
1132	137	7.6	517	1	PVR1_HUMAN	Q8jhl6	rattus norv	1205	133	7.4	323	2	Q9ESA2	Q9esa2	rattus norv
1133	137	7.6	662	2	Q8MQD9	Q15223	homo sapien	1206	133	7.4	366	2	Q9N680	Q9n680	drosophila
1134	137	7.6	662	2	Q8MQD9	Q8mqd9	drosophila	1207	133	7.4	383	2	Q18431	Q18431	geodia cydo
1135	137	7.6	778	1	TRKA_CHICK	Q9vgd0	drosophila	1208	133	7.4	541	2	Q95XJ7	Q95xj7	caenorhabdi
1136	137	7.6	977	2	Q98S12	Q1009	gallus galli	1209	133	7.4	612	2	Q96CY4	Q96cy4	homo sapien
1137	136.5	7.6	345	2	Q7PVU1	Q98su2	danio kerri	1210	133	7.4	802	1	FGRA_HUMAN	Q96cy4	homo sapien
1138	136.5	7.6	459	2	Q8EX391	Q8ex391	homo sapien	1211	133	7.4	802	2	Q8TDA0	Q8tda0	homo sapien
1139	136.5	7.6	498	2	Q9UBF9	Q9ubf9	homo sapien	1212	133	7.4	807	2	Q6DD66	Q6dd66	homo sapien
1140	136.5	7.6	677	2	Q8QHL2	Q8qhl2	gallus galli	1213	133	7.4	818	2	Q91742	Q91742	homo sapien
1141	136.5	7.6	738	1	PEC1_HUMAN	Q16284	homo sapien	1214	133	7.4	818	2	Q9PSV9	Q9psv9	homo sapien
1142	136.5	7.6	3100	2	Q7KYN5	Q7kyn5	homo sapien	1215	133	7.4	839	1	TRKC_HUMAN	Q16288	homo sapien
1143	136	7.5	229	2	Q7Q984	Q7q984	anopheles g	1216	133	7.4	839	2	Q75682	Q75682	homo sapien
1144	136	7.5	298	2	Q8C5K9	Q8c5k9	mus musculus	1217	133	7.4	974	2	Q98S03	Q98s03	danio dangi
1145	136	7.5	298	2	Q8CE95	Q8ce95	mus musculus	1218	133	7.4	1091	2	Q9YH41	Q9yh41	gallus galli
1146	136	7.5	298	2	Q9J159	Q9j159	m vascular	1219	132.5	7.3	393	2	P97547	P97547	rattus norv
1147	136	7.5	393	2	Q95727	Q95727	homo sapien	1220	132.5	7.3	411	2	Q15228	Q15228	homo sapien
1148	136	7.5	903	2	Q8N9C0	Q8n9c0	homo sapien	1221	132.5	7.3	419	2	Q68CR6	Q68cr6	homo sapien
1149	136	7.5	976	2	Q8JFR5	Q8jfr5	brachydanio	1222	132.5	7.3	439	2	Q6P520	Q6p520	homo sapien
1150	135.5	7.5	326	2	Q9PU18	Q9pu18	anopheles g	1223	132.5	7.3	423	2	Q8BU57	Q8bu57	mus musculus
1151	135.5	7.5	326	2	Q9PU18	Q9n166	papio hamad	1224	132.5	7.3	426	1	PSG8_HUMAN	Q9uq74	homo sapien
1152	135.5	7.5	442	2	Q7PT04	Q7pt04	anopheles g	1225	132.5	7.3	492	2	Q7QDf4	Q7qd44	anopheles g
1153	135.5	7.5	762	2	Q71TW8	Q71tw8	homo sapien	1226	132.5	7.3	533	2	Q8NCB6	Q8ncb6	homo sapien
1154	135.5	7.5	822	2	Q91288	Q91288	pleurodeles	1227	132.5	7.3	534	2	Q8NB18	Q8nb18	homo sapien
1155	135.5	7.5	975	2	Q79750	P79750	fugu rubrip	1228	132.5	7.3	584	2	Q90989	Q90989	gallus galli
1156	135.5	7.5	13133	2	Q71A42	Q71a42	caenorhabdi	1229	132.5	7.3	620	2	Q61GL3	Q61gl3	drosophila
1157	135	7.5	332	2	Q640U3	Q640u3	homo sapien	1230	132.5	7.3	626	2	Q90880	Q90880	gallus galli
1158	135	7.5	393	2	Q61RX2	Q61rx2	homo sapien	1231	132.5	7.3	671	2	Q63711	Q63711	rattus ratt
1159	135	7.5	464	2	Q6GL25	Q6gl25	homo sapien	1232	132.5	7.3	800	2	Q9JHX9	Q9jhx9	rattus norv
1160	135	7.5	802	2	Q95M13	Q95m13	bos taurus	1233	132.5	7.3	856	2	Q62121	Q62121	mus musculus
1161	135	7.5	817	2	Q8JG38	Q8jg38	brachydanio	1234	132.5	7.3	1087	2	Q9PUF6	Q9puF6	gallus galli
1162	134.5	7.4	242	2	Q46604	Q46604	mus musculus	1235	132	7.3	201	2	Q7PX42	Q7px42	anopheles g
1163	134.5	7.4	263	2	Q7TPW5	Q7tpw5	mus musculus	1236	132	7.3	387	2	Q86XK7	Q86xk7	homo sapien
1164	134.5	7.4	348	2	Q8FN3	Q8fn3	homo sapien	1237	132	7.3	408	2	Q8K094	Q8k094	m hypotheti
1165	134.5	7.4	419	1	PSG7_HUMAN	Q13046	homo sapien	1238	132	7.3	412	2	Q6MZS4	Q6mz44	homo sapien
1166	134.5	7.4	426	2	Q64HX5	Q64hx5	oncorhynch	1239	132	7.3	502	2	Q9Z2Q0	Q9z2q0	mus musculus
1167	134.5	7.4	428	1	PSG3_HUMAN	Q16557	homo sapien	1240	132	7.3	582	2	Q95N25	Q95n25	bos taurus
1168	134.5	7.4	480	2	Q9PSD1	Q9psd1	homo sapien	1241	132	7.3	992	2	Q8AXU0	Q8axu0	oncorhynch
1169	134.5	7.4	493	2	Q6P5Y4	Q6p5y4	homo sapien	1242	132	7.3	1048	2	P79749	P79749	fugu rubrip
1170	134.5	7.4	531	2	Q659F2	Q659f2	homo sapien	1243	131.5	7.3	298	1	JAM2_HUMAN	P57087	homo sapien
1171	134.5	7.4	659	2	Q6ZNM1	Q6znm1	homo sapien	1244	131.5	7.3	298	2	Q6VNC1	Q6vnc1	homo sapien
1172	134.5	7.4	660	2	Q7Z681	Q7z681	homo sapien	1245	131.5	7.3	312	2	Q6UXG6	Q6uxg6	homo sapien
1173	134.5	7.4	782	2	Q80T08	Q80t08	mus musculus	1246	131.5	7.3	370	2	Q6MZQ3	Q6mzq3	homo sapien
1174	134.5	7.4	1205	2	Q8BUJ0	Q8buJ0	mus musculus	1247	131.5	7.3	480	2	Q9PSC9	Q9psc9	homo sapien
1175	134.5	7.4	1235	2	Q95428	Q95428	homo sapien	1248	131.5	7.3	739	2	Q865F2	Q865f2	oryctolagus
1176	134.5	7.4	19066	2	Q801W8	Q801w8	brachydanio	1249	131.5	7.3	814	2	Q6GNP8	Q6gnp8	homo sapien
1177	134	7.4	217	2	Q6KGN0	Q6kgn0	bacterioph	1250	131	7.3	259	2	Q8WR47	Q8wr47	caenorhabdi
1178	134	7.4	238	2	Q20339	Q20339	caenorhabdi	1251	131	7.3	298	2	Q9GL74	Q9gl74	cercopithe
1179	134	7.4	283	2	Q9VKN0	Q9vkn0	drosophila	1252	131	7.3	327	2	Q961Q7	Q961q7	homo sapien
1180	134	7.4	294	2	Q6KGN1	Q6kgn1	bacterioph	1253	131	7.3	330	2	Q63241	Q63241	rattus norv
1181	134	7.4	321	2	Q9DEE6	Q9dee6	gallus galli	1254	131	7.3	342	2	Q9ESA1	Q9esa1	rattus norv
1182	134	7.4	397	2	Q6XRC3	Q6xrc3	homo sapien	1255	131	7.3	355	2	Q7Q1W7	Q7q1w7	anopheles g
1183	134	7.4	486	2	Q9DEE4	Q9dee4	gallus galli	1256	131	7.3	408	2	Q91WP1	Q91wp1	mus musculus
1184	134	7.4	533	2	Q9DEE5	Q9dee5	gallus galli	1257	131	7.3	408	2	Q8BVf6	Q8bvF6	mus musculus
1185	134	7.4	612	2	Q9Z2P9	Q9z2p9	mus musculus	1258	131	7.3	429	2	Q6VAN7	Q6van7	bos taurus
1186	134	7.4	825	2	Q6VNS1	Q6vns1	mus musculus	1259	131	7.3	782	2	Q9ESAS	Q9esAs	rattus norv
1187	134	7.4	864	1	TRKC_RAT	Q03351	rattus norv	1260	131	7.3	935	2	Q64OT5	Q64ot5	homo sapien
1188	134	7.4	1147	1	KMLS_RABIT	P29294	oryctolagus	1261	131	7.3	978	1	Q9XS93	Q9xs93	canis fami
1189	133.5	7.4	283	2	Q7QK74	Q7qk74	anopheles g	1262	131	7.3	1097	1	PGDR_RAT	Q05030	rattus norv
1190	133.5	7.4	289	2	Q9Q1L5	Q9q1l5	mus musculus	1263	131	7.3	1106	1	PGDR_HUMAN	F09619	homo sapien
1191	133.5	7.4	332	2	Q6P359	Q6p359	homo sapien	1264	130.5	7.2	295	2	Q9GL75	Q9gl75	bos taurus
1192	133.5	7.4	335	1	PSG2_HUMAN	P11465	homo sapien	1265	130.5	7.2	295	2	Q9QYL6	Q9qyl6	mus musculus
1193	133.5	7.4	374	2	Q7Q5J8	Q7qb18	anopheles g	1266	130.5	7.2	295	2	Q9Z2H8	Q9z2h8	mus musculus
1194	133.5	7.4	584	2	Q98921	Q98921	gallus galli	1267	130.5	7.2	310	1	FCGB_HUMAN	P31994	homo sapien
1195	133.5	7.4	597	1	SILL_PANTR	Q951h0	pan troglod	1268	130.5	7.2	323	1	FCGC_HUMAN	P31995	homo sapien
1196	133.5	7.4	626	2	Q98922	Q98922	gallus galli	1269	130.5	7.2	385	1	BAS1_HUMAN	P35613	homo sapien
1197	133.5	7.4	729	1	FGRI_DROME	Q07407	drosophila	1270	130.5	7.2	523	2	Q80ZE2	Q80ze2	mus musculus
1198	133.5	7.4	755	2	Q8CCF8	Q8ccf8	mus musculus	1271	130.5	7.2	569	1	SILF_MOUSE	Q920g3	mus musculus
1199	133.5	7.4	879	2	Q6PE80	Q6pe80	mus musculus	1272	130.5	7.2	707	2	Q9TT07	Q9tt07	canis fami

1273	130.5	7.2	775	2	O97754	O97754	oryctolagus	1346	126.5	7.0	722	2	O6GNB3	O6gnb3	xenopus lae
1274	130.5	7.2	873	2	O98949	O98949	gallus gall	1347	126.5	7.0	723	2	O86Y14	O86y14	homo sapien
1275	130	7.2	325	2	O95791	O95791	homo sapien	1348	126.5	7.0	945	2	O77589	O77589	equus cabal
1276	130	7.2	332	1	CD22_PANPA	O91e5	pan paniscu	1349	126.5	7.0	1099	2	O7TMR8	O7tmr8	mus musculus
1277	130	7.2	332	1	CD22_PANTR	O91e6	pan troglod	1350	126.5	7.0	1212	2	O95TG0	O95tg0	drosophila
1278	130	7.2	394	2	O925F2	O925f2	mus musculus	1351	126	7.0	168	2	O8MI25	O8mi25	ovis aries
1279	130	7.2	697	2	O922E0	O922e0	mus musculus	1352	126	7.0	204	2	O8MZH7	O63zh7	xenopus lae
1280	130	7.2	732	1	PEC1_MOUSE	O98481	mus musculus	1353	126	7.0	553	2	O8WXJ5	O8wxj5	homo sapien
1281	130	7.2	727	2	O8CWA4	O8caw4	mus musculus	1354	126	7.0	822	1	TRKB_HUMAN	O16620	homo sapien
1282	129.5	7.2	208	2	O866T1	O866t1	pongo pygma	1355	126	7.0	828	2	O9DGK3	O9dgk3	xenopus lae
1283	129.5	7.2	272	2	O7Q1Q2	O7qlq2	drosophila	1356	126	7.0	838	2	O8WXJ7	O8wxj7	homo sapien
1284	129.5	7.2	346	2	P92027	P92027	drosophila	1357	125.5	6.9	251	2	O09970	O09970	caenorhabdi
1285	129.5	7.2	365	2	O6VAN5	O6van5	bos taurus	1358	125.5	6.9	278	2	O61350	O61350	mus musculus
1286	129.5	7.2	372	2	O6VAN6	O6van6	bos taurus	1359	125.5	6.9	341	2	O61353	O61353	mus musculus
1287	129.5	7.2	415	2	O60977	O60977	canis famill	1360	125.5	6.9	342	2	P97635	P97635	rattus norv
1288	129.5	7.2	436	2	O6VAN8	O6van8	bos taurus	1361	125.5	6.9	524	2	O8IOV7	O8ioV7	dugesia jap
1289	129.5	7.2	582	2	O80WN2	O80wn2	mus musculus	1362	125.5	6.9	525	2	O9W0L9	O9w0l9	drosophila
1290	129.5	7.2	595	2	O68SN8	O68sn8	mus musculus	1363	125.5	6.9	526	1	BUTY_HUMAN	O13410	homo sapien
1291	129.5	7.2	771	2	O8N116	O8n116	homo sapien	1364	125.5	6.9	787	2	O8K061	O8k061	mus musculus
1292	129.5	7.2	967	2	O76KE8	O76ke8	oncorhynch	1365	125.5	6.9	829	2	O9PSV8	O9psv8	xenopus lae
1293	129.5	7.2	975	1	KIT_CANFA	O97799	canis famill	1366	125.5	6.9	975	1	KIT_MOUSE	O05532	mus musculus
1294	129.5	7.2	975	2	O7YRV7	O7yrv7	canis famill	1367	125.5	6.9	975	1	O6QJB7	O6qjb7	mus musculus
1295	129.5	7.2	979	2	O8WN23	O8wn23	canis famill	1368	125.5	6.9	975	2	O6QJB8	O6qjb8	mus musculus
1296	129.5	7.2	987	2	O7YZM8	O7yzm8	caenorhabdi	1369	125.5	6.9	975	2	O7TS86	O7ts86	mus musculus
1297	129.5	7.2	1040	1	EG15_CAEEL	O16556	caenorhabdi	1370	125.5	6.9	979	2	O8C8K9	O8c8k9	mus musculus
1298	129.5	7.2	1051	2	O7JL68	O7jl68	caenorhabdi	1371	125.5	6.9	1031	2	O80YN7	O80yn7	mus musculus
1299	129.5	7.2	1096	2	O8MQ14	O8mq14	caenorhabdi	1372	125.5	6.9	10578	2	O8ISF5	O8isf5	caenorhabdi
1300	129	7.1	306	2	O9QY14	O9qy14	mus musculus	1373	125	6.9	370	2	O7TSN7	O7tsn7	mus musculus
1301	129	7.1	321	2	O9DEE3	O9dee3	gallus gall	1374	125	6.9	398	2	O9Y640	O9y640	homo sapien
1302	129	7.1	328	2	O6ZMC9	O6zmc9	homo sapien	1375	125	6.9	707	2	O8CB6	O8cb6	mus musculus
1303	129	7.1	417	1	PVR_HUMAN	P15151	homo sapien	1376	125	6.9	876	2	O7PW78	O7pw78	anopheles g
1304	129	7.1	486	2	O9DEE2	O9dee2	gallus gall	1377	125	6.9	964	2	O9TQ00	O9tq00	sus scrofa
1305	129	7.1	533	2	O9DEE1	O9dee1	gallus gall	1378	125	6.9	977	1	KIT_BOVIN	P43481	bos taurus
1306	129	7.1	1098	1	PGDR_MOUSE	O95622	mus musculus	1379	125	6.9	978	1	KIT_CAPH1	O28317	capra hircu
1307	128.5	7.1	213	2	O9N167	O9n167	papio hamad	1380	125	6.9	1062	2	O8A3C7	O8axc7	fugu rubrip
1308	128.5	7.1	226	2	O7PYG1	O7pyg1	anopheles g	1381	125	6.9	1078	2	O8AXC8	O8axc8	fugu rubrip
1309	128.5	7.1	268	2	O4603	O4603	sus scrofa	1382	124.5	6.9	145	2	O9MZE4	O9mze4	macaca mula
1310	128.5	7.1	477	2	O6UXJ4	O6uxj4	homo sapien	1383	124.5	6.9	192	2	O9ERP7	O9erp7	rattus norv
1311	128.5	7.1	515	1	PVR1_MOUSE	O9j1kf6	mus musculus	1384	124.5	6.9	244	2	O95T89	O95t89	drosophila
1312	128.5	7.1	515	2	O6P9M9	O6p9m9	mus musculus	1385	124.5	6.9	311	2	O6DN73	O6dn73	homo sapien
1313	128.5	7.1	593	1	SILL_HUMAN	O96pq1	homo sapien	1386	124.5	6.9	496	2	O6ZTG1	O6ztg1	homo sapien
1314	128.5	7.1	733	2	O9QZM7	O9qzm7	mus musculus	1387	124.5	6.9	499	2	O7Z728	O7z728	homo sapien
1315	128	7.1	240	2	O6TYZ5	O6tyz5	canis famill	1388	124.5	6.9	504	2	O98923	O98923	gallus gall
1316	128	7.1	319	2	O7YU80	O7yu80	canis famill	1389	124.5	6.9	731	2	O91150	O91150	notophthalm
1317	128	7.1	769	2	O8N115	O8n115	homo sapien	1390	124.5	6.9	828	2	O91743	O91743	xenopus lae
1318	128	7.1	806	1	FR3_HUMAN	P22607	homo sapien	1391	124.5	6.9	960	1	KIT_CHICK	O08156	gallus gall
1319	128	7.1	1129	2	O80UX0	O80ux0	mus musculus	1392	124	6.9	259	2	O7Z2Q1	O7z2q1	homo sapien
1320	128	7.1	1214	2	O75054	O75054	homo sapien	1393	124	6.9	278	2	O99232	O99232	mus musculus
1321	128	7.1	1427	2	O9VZT8	O9vzt8	drosophila	1394	124	6.9	341	2	O61354	O61354	mus musculus
1322	127.5	7.1	94	2	O9VR14	O9vr14	drosophila	1395	124	6.9	426	1	PSG9_HUMAN	O00887	homo sapien
1323	127.5	7.1	241	2	O07112	O07112	bos taurus	1396	124	6.9	650	2	O63709	O63709	rattus sp.
1324	127.5	7.1	271	1	OX2V_HHV8	P88963	human herpe	1397	124	6.9	812	2	O69ZJ6	O69zj6	mus musculus
1325	127.5	7.1	329	2	O40948	O40948	human herpe	1398	124	6.9	972	2	O26614	O26614	strongyloce
1326	127.5	7.1	329	2	O9Z178	O9z178	mus musculus	1399	124	6.9	993	1	FLT3_HUMAN	P36888	homo sapien
1327	127.5	7.1	388	1	BASI_RAT	P26453	rattus norv	1400	124	6.9	999	1	MERK_HUMAN	O12866	homo sapien
1328	127.5	7.1	390	2	O95KIT3	O95ki3	macaca fasc	1401	124	6.9	1124	2	O6P6L5	O6p6l5	mus musculus
1329	127.5	7.1	499	1	SIL8_HUMAN	O9nyz4	homo sapien	1402	124	6.9	1294	2	O80T80	O80t80	mus musculus
1330	127.5	7.1	926	2	O7LDM3	O7ldm3	homo sapien	1403	124	6.9	1569	2	O6PAC0	O6pac0	mus musculus
1331	127	7.0	330	1	CD22_PONPY	O9n1e3	pongo pygma	1404	124	6.9	1666	1	MYM1_MOUSE	O26234	mus musculus
1332	127	7.0	406	2	O8BR20	O8br20	mus musculus	1405	123.5	6.8	181	2	O91665	O91665	xenopus lae
1333	127	7.0	452	2	O70355	O70355	mus musculus	1406	123.5	6.8	211	2	O8BK18	O8bk18	mus musculus
1334	127	7.0	595	2	O90720	O90720	gallus gall	1407	123.5	6.8	231	2	O8WYI6	O8wyi6	homo sapien
1335	127	7.0	658	2	O8NHN4	O8nhn4	homo sapien	1408	123.5	6.8	241	2	O6PK61	O6pk61	homo sapien
1336	127	7.0	879	1	FRP_MOUSE	O9wv91	mus musculus	1409	123.5	6.8	253	2	O9D8H2	O9d8h2	m mus muscu
1337	127	7.0	992	1	FLT3_MOUSE	O00342	mus musculus	1410	123.5	6.8	257	2	O8R202	O8r202	mus musculus
1338	126.5	7.0	295	2	O9ERF5	O9erf5	mesocricetu	1411	123.5	6.8	261	2	O9D7L8	O9d7l8	m mus muscu
1339	126.5	7.0	305	2	O6ZS95	O6zs95	homo sapien	1412	123.5	6.8	285	2	O9D780	O9d780	mus musculus
1340	126.5	7.0	340	2	O6ZS95	O6zs95	homo sapien	1413	123.5	6.8	285	2	O8VE93	O8ve93	mus musculus
1341	126.5	7.0	344	2	O9UKV4	O9ukv4	homo sapien	1414	123.5	6.8	357	2	O8SEW5	O8spw5	macaca fasc
1342	126.5	7.0	365	1	CXAR_HUMAN	P78310	homo sapien	1415	123.5	6.8	402	2	O15227	O15227	homo sapien
1343	126.5	7.0	466	2	O95S10	O95s10	drosophila	1416	123.5	6.8	403	2	O8HY15	O8hy15	lemur catta
1344	126.5	7.0	516	2	O6PHF8	O6phf8	brachydanio	1417	123.5	6.8	501	2	O6GMJ2	O6gmj2	brachydanio
1345	126.5	7.0	677	1	NRG1_XENLA	O93383	xenopus lae	1418	123.5	6.8	516	2	O6NW94	O6nw94	brachydanio



1419	123.5	6.8	574	1	IRL2_MOUSE	Q9ers7	mus musculus	Q9negl drosophila
1420	123.5	6.8	640	1	DM1_CABEL	Q18066	caenorhabdi	Q14324 homo sapien
1421	123.5	6.8	645	2	Q6DR98	Q6dr98	mus musculus	Q7pt57 anopheles g
1422	123.5	6.8	978	1	KIT_FELCA	Q28889	felis silve	Q9nx42 homo sapien
1423	123.5	6.8	1349	1	G116_RAT	Q9wvt0	rattus norv	Q8ve98 mus musculus
1424	123	6.8	168	2	Q7Q6K5	Q7qkx5	anopheles g	Q7tpb4 rattus norv
1425	123	6.8	287	2	Q9QW80	Q9qw80	mus sp. f	Q63242 rattus norv
1426	123	6.8	321	2	Q6UX14	Q6ux14	homo sapien	Q35947 mesoicetu
1427	123	6.8	351	2	Q15225	Q15225	homo sapien	Q6pj50 mus musculus
1428	123	6.8	367	2	Q8T603	Q8t603	drosophila	
1429	123	6.8	399	2	Q9Y279	Q9y279	homo sapien	
1430	123	6.8	476	2	Q80WU0	Q80wu0	mus musculus	
1431	123	6.8	696	1	IPL1_HUMAN	Q9nzn1	homo sapien	
1432	123	6.8	696	1	IPL1_PANTR	P60029	pan troglod	
1433	123	6.8	707	2	P97860	P97860	mus musculus	
1434	123	6.8	821	1	TRKB_MOUSE	P15209	mus musculus	
1435	123	6.8	1072	2	Q8T104	Q8t104	bombyx mori	
1436	123	6.8	1176	1	KMLS_BOVIN	Q28824	bos taurus	
1437	122.5	6.8	167	2	Q8NFN2	Q8nfn2	homo sapien	
1438	122.5	6.8	211	2	Q7RTW5	Q7rtw5	homo sapien	
1439	122.5	6.8	241	1	Q7RTW0	Q7rtw0	homo sapien	
1440	122.5	6.8	316	1	FCGA_PANTR	Q8spv8	pan troglod	
1441	122.5	6.8	326	1	VB16_CWXPB	Q04523	cowpox viru	
1442	122.5	6.8	326	2	Q77DR6	Q77dr6	cowpox viru	
1443	122.5	6.8	394	2	Q6TGK9	Q6tgk9	oryctolagus	
1444	122.5	6.8	412	2	Q9R1E1	Q9r1e1	rattus norv	
1445	122.5	6.8	462	2	Q7RTW1	Q7rtw1	homo sapien	
1446	122.5	6.8	637	2	Q7RTW3	Q7rtw3	homo sapien	
1447	122.5	6.8	639	1	NRG1_HUMAN	Q02297	h pro-neure	
1448	122.5	6.8	640	2	Q7RTV8	Q7rtv8	homo sapien	
1449	122.5	6.8	645	2	Q7RTW4	Q7rtw4	homo sapien	
1450	122.5	6.8	662	1	NRG1_RAT	P43322	r pro-neure	
1451	122.5	6.8	785	2	Q7TNP4	Q7tnp4	mus musculus	
1452	122.5	6.8	994	1	MERK_RAT	P57097	rattus norv	
1453	122	6.8	272	2	Q8RLN5	Q8rln5	mus musculus	
1454	122	6.8	390	2	Q7QBR2	Q7qbr2	anopheles g	
1455	122	6.8	397	2	Q09263	Q09263	cercopithe	
1456	122	6.8	458	1	CD4_MACFA	P79185	macaca fasc	
1457	122	6.8	459	2	Q6ZMD0	Q6zmd0	homo sapien	
1458	122	6.8	606	2	Q9BZ20	Q9bz20	homo sapien	
1459	122	6.8	696	1	IPL1_PONPY	Q7yq19	pongo pygma	
1460	122	6.8	696	1	IPL1_RAT	P59824	rattus norv	
1461	122	6.8	850	1	NRG2_HUMAN	O14511	homo sapien	
1462	122	6.8	923	2	Q97745	Q97745	sus scrofa	
1463	122	6.8	953	2	Q6P6Y9	Q6p6y9	xenopus lae	
1464	122	6.8	964	2	Q97744	Q97744	sus scrofa	
1465	122	6.8	964	2	Q9TQ01	Q9tq01	sus scrofa	
1466	122	6.8	1685	2	Q6H969	Q6h969	homo sapien	
1467	122	6.8	1685	2	Q6ZUU0	Q6zuu0	homo sapien	
1468	121.5	6.7	155	2	Q9JJ17	Q9jj17	mus musculus	
1469	121.5	6.7	305	2	Q6RPJ0	Q6rpj0	homo sapien	
1470	121.5	6.7	332	1	PSGB_HUMAN	Q9uq72	homo sapien	
1471	121.5	6.7	365	2	Q8WMV3	Q8wmv3	bos taurus	
1472	121.5	6.7	390	2	Q96AP7	Q96ap7	homo sapien	
1473	121.5	6.7	390	2	Q96T50	Q96t50	homo sapien	
1474	121.5	6.7	412	2	Q63611	Q63611	rattus norv	
1475	121.5	6.7	558	2	Q6PDB1	Q6pdb1	homo sapien	
1476	121.5	6.7	637	2	Q6NSG0	Q6nsg0	homo sapien	
1477	121.5	6.7	818	1	TRKB_CHICK	Q91987	gallus gall	
1478	121.5	6.7	821	1	TRKB_RAT	Q63604	rattus norv	
1479	121.5	6.7	1450	1	MPSF_CHICK	Q02173	gallus gall	
1480	121	6.7	223	2	Q9NBC0	Q9nbc0	drosophila	
1481	121	6.7	277	2	Q61ER8	Q61er8	rattus norv	
1482	121	6.7	281	2	P97546	P97546	rattus norv	
1483	121	6.7	292	2	Q9N168	Q9n168	papio hamad	
1484	121	6.7	292	2	O57146	O57146	human herpe	
1485	121	6.7	292	2	Q78517	Q78517	human herpe	
1486	121	6.7	303	2	Q7ZXR4	Q7zxr4	xenopus lae	
1487	121	6.7	305	2	Q6P3A4	Q6p3a4	mus musculus	
1488	121	6.7	532	2	Q95R30	Q95r30	drosophila	
1489	121	6.7	733	2	Q6O830	Q6o830	mus musculus	
1490	121	6.7	733	2	Q80T10	Q80t10	mus musculus	
1491	121	6.7	994	1	MERK_MOUSE	Q60805	mus musculus	
1492	121	6.7	1035	2	Q9NEG1	Q9neg1	drosophila	
1493	121	6.7	1142	1	MYPE_HUMAN	Q14324	homo sapien	
1494	121	6.7	1333	2	Q7PT57	Q7pt57	anopheles g	
1495	120.5	6.7	284	2	Q9NX42	Q9nx42	homo sapien	
1496	120.5	6.7	316	2	Q8VE98	Q8ve98	mus musculus	
1497	120.5	6.7	316	2	Q7TPB4	Q7tpb4	rattus norv	
1498	120.5	6.7	353	2	Q63242	Q63242	rattus norv	
1499	120.5	6.7	461	2	Q35947	Q35947	mesoicetu	
1500	120.5	6.7	468	2	Q6PJ50	Q6pj50	mus musculus	
RESULT 1								ALIGNMENTS
Q8BG33	ID	Q8BG33	PRELIMINARY;	PRT;	344 AA.			
AC	Q8BG33;							
DT	01-MAR-2003 (T-EMBLrel. 23, Created)							
DT	01-MAR-2003 (T-EMBLrel. 23, Last sequence update)							
DT	05-JUL-2004 (T-EMBLrel. 27, Last annotation update)							
DE	Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length							
DE	enriched library, clone:B230328N06 product:NEUOTRIMIN (GP65) homolog							
DE	(Mus musculus adult male corpora quadrigemina cDNA, RIKEN full-length							
DE	enriched library, clone:B230377K17 product:NEUOTRIMIN (GP65)							
DE	homolog.)							
GN	Name=Hnt;							
OS	Mus musculus (Mouse).							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.							
OX	NCBI_TaxID=10090;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;							
RX	MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;							
RA	Carninci P., Hayashizaki Y.;							
RT	"High-efficiency full-length cDNA cloning.";							
RL	Meth. Enzymol. 303:19-44(1999).							
RN	[2]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;							
RX	MEDLINE=21085650; PubMed=11217851; DOI=10.1038/35055500;							
RA	RIKEN FANTOM Consortium;							
RT	"Functional annotation of a full-length mouse cDNA collection.";							
RL	Nature 409:685-690(2001).							
RN	[3]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;							
RA	The FANTOM Consortium.							
RT	the RIKEN Genome Exploration Research Group Phase I & II Team;							
RL	"Analysis of the mouse transcriptome based on functional annotation of							
RT	60,770 full-length cDNAs.";							
RL	Nature 420:563-573(2002).							
RN	[4]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;							
RX	MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;							
RA	Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,							
RA	Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;							
RT	"Normalization and subtraction of cap-trapper-selected cDNAs to							
RT	prepare full-length cDNA libraries for rapid discovery of new genes.";							
RL	Genome Res. 10:1617-1630(2000).							
RN	[5]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=C57BL/6J; TISSUE=Corpora quadrigemina;							
RX	MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;							
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,							
RA	Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,							
RA	Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,							
RA	Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,							
RA	Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,							
RA	Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,							
RA	Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,							
RA	Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;							



```

CC -----
DR EMBL: AF126426; AAF37591.1; -
DR EMBL: AY358331; AAQ88697.1; -
DR EMBL: BC050716; AAH50716.1; -
DR HSP; P13590; 1IE5.
DR MIM; 607938; -
DR GO; GO:0008038; P:neural cell recognition; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS0835; IG_LIKE; 3.
DR Alternative splicing; Cell adhesion; Direct protein sequencing;
KW Glycoprotein; GPI-anchor; Immunoglobulin domain; Lipoprotein; Repeat;
KW SIGNAL.
FT SIGNAL 1 33 Neurotrimin.
FT CHAIN 34 321
FT PROPEP 322 344 Removed in mature form (Potential).
FT DOMAIN 39 126 Ig-like C2-type 1.
FT DOMAIN 136 218 Ig-like C2-type 2.
FT DOMAIN 222 309 Ig-like C2-type 3.
FT DISULFID 57 115 Potential.
FT DISULFID 157 201 Potential.
FT DISULFID 243 295 Potential.
FT CARBOHYD 44 44 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 70 70 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 152 152 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 284 284 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 292 292 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 305 305 N-linked (GLCNAC. .) (Potential).
FT CARBOHYD 321 321 N-linked (GLCNAC. .) (Potential).
FT LIPID 321 321 GPI-anchor amidated asparagine (Potential).
FT VARSPLIC 1 27 MGCVGLFLPWKLKLVVLSRLFLVPT -> MKTIQPIQMN
FT SLSWAIFTLGLAALCLFQ (in isoform 2).
FT FTID=VSP_010939.
FT PGAV -> ETVL (in isoform 3).
FT FTID=VSP_010940.
FT Missing (in isoform 3).
FT FTID=VSP_010941.
FT FTID=VSP_010941.
FT SSEQUENCE 344 AA; 37971 MW; DA4D12C395ABBE3A CRC64;
Query Match 92.2%; Score 1665.5; DB 1; Length 344;
Best Local Similarity 95.2%; Pred. No. 1.9e-124;
Matches 320; Conservative 3; Mismatches 10; Indels 3; Gaps 1;
QY 12 ISWAIFTLGLAALCLF--QGVPRSGDATPPKAMDNVTVRQGSATLRCITIDNRVTRVAV 68
Db 9 LPWKCLVVSRLFLVPTGVPVRSRGDATPPKAMDNVTVRQGSATLRCITIDNRVTRVAV 68
QY 69 LNRSTILYAGNDKWCIDPRVLLSNTQYISIQNVVDYDEGPTCSVQTDNHPKTSRV 128
Db 69 LNRSTILYAGNDKWCIDPRVLLSNTQYISIQNVVDYDEGPTCSVQTDNHPKTSRV 128
QY 129 HLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVTRHISPKAVGFVSEDEYLEI 188
Db 129 HLIVQVSPKIVEISSDISINEGNNISLTCTIATGRPEPTVTRHISPKAVGFVSEDEYLEI 188
QY 189 QGITRQSGDYECASNDVAAPVRRVKVTVNTPYIYSEAKGTGVPVQKGTLCQCSASAV 248
Db 189 QGITRQSGDYECASNDVAAPVRRVKVTVNTPYIYSEAKGTGVPVQKGTLCQCSASAV 248
QY 249 PSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLIGHTNASI 308
Db 249 PSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLIGHTNASI 308
QY 309 MLFGPGAVSEVSGTSSRACGVWLLPLLVLLHLKLF 344
Db 309 MLFGPGAVSEVSGTSSRACGVWLLPLLVLLHLKLF 344
RESULT 3
NTRI_MOUSE

```

```

ID AC Q99PJ0; STANDARD; PRT; 344 AA.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neurotrimin precursor.
GN Name=Nt; Synonyms=Hnt;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=Brain;
RA Kim T.H., Choi S.C., Kim J., Jeon J.W., Kim K.D., Lee S.H.;
RT "Cloning and expression of mouse neurotrimin gene in the developing
RL nervous system.";
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedtin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Touchman J.W., Green E.D., Dickinson M.C.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Neural cell adhesion molecule.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON
family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF282980; AAK00276.1; -
DR EMBL: BC023307; AAH23307.1; -
DR MGD; MGI:2446259; Hnt.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS0835; IG_LIKE; 3.
KW Cell adhesion; Glycoprotein;
KW Lipoprotein; Repeat; Signal.
FT SIGNAL 1 33 Potential.
FT CHAIN 34 321 Neurotrimin.
FT PROPEP 322 344 Removed in mature form (Potential).
FT DOMAIN 39 126 Ig-like C2-type 1.
FT DOMAIN 136 218 Ig-like C2-type 2.
FT DOMAIN 222 309 Ig-like C2-type 3.
FT DISULFID 57 115 Potential.

```

```

FT DISULFID 157 201 Potential.
FT DISULFID 243 295 Potential.
FT CARBOHYD 44 44 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 70 70 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 152 152 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 284 284 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 292 292 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 305 305 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 321 321 N-linked (GlcNAc... ) (Potential).
FT LIPID 321 321 GPI-anchor amidated asparagine (Potential).
FT CONFLICT 75 75 L -> P (in Ref. 1).
FT CONFLICT 92 92 S -> G (in Ref. 1).
FT CONFLICT 119 119 T -> I (in Ref. 1).
FT CONFLICT 187 187 E -> Q (in Ref. 1).
FT CONFLICT 213 213 R -> P (in Ref. 1).
FT CONFLICT 225 225 I -> F (in Ref. 1).
SQ SEQUENCE 344 AA; 37984 MW; C885BBA52C148554 CRC64;

Query Match 91.2%; Score 1647.5; DB 1; Length 344;
Best Local Similarity 93.5%; Pred. No. 5.3e-123;
Matches 314; Conservative 8; Mismatches 11; Indels 3; Gaps 1;

QY 12 ISWAIFTGLAALCLF---QGVPRVSGDATFPKAMDNVTVRQGESATLRCITDNRVTRVAV 68
Db 9 LPWKCLVVSLRLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCITDNRVTRVAV 68
QY 69 LNRSTLYAGNDKWCLDPRVLLSNTQYSIEIQNVVDVDEGPTCSVQTDNHPKTSRV 128
Db 69 LNRSTLYAGNDKWCLDPRVLLSNTQYSIEIQNVVDVDEGPTCSVQTDNHPKTSRV 128
QY 129 HLIVQSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEI 188
Db 129 HLIVQSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEI 188
QY 189 QGITREOSGDYECASNDVAAPVRRVKVTNVPYPISEAKGTGVPVGQGTIQCEASAV 248
Db 189 QGITREOSGDYECASNDVAAPVRRVKVTNVPYPISEAKGTGVPVGQGTIQCEASAV 248
QY 249 PSAEFQWKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTASI 308
Db 249 PSAEFQWKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTASI 308
QY 309 MLFGPGAVSEVNGTSRRAGCIVLLPLLVHLHLK 344
Db 309 MLFGPGAVSEVNGTSRRAGCIVLLPLLVHLHLK 344

RESULT 4
NTRI_RAT NTRI_RAT STANDARD; PRT; 344 AA.
AC Q62718;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Neurotrophin precursor (Gp65).
GN Name=Nt;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RC SEQUENCE FROM N.A., AND SEQUENCE OF 217-229.
RP STRAIN=Sprague-Dawley;
RX MEDLINE=95198094; PubMed=7891157;
RA Struyk A.F., Canoll P.D., Wolfgang M.J., Rosen C.L., D'Eustachio P.,
RA Salzer J.L.;
RT "Cloning of neurotrophin defines a new subfamily of differentially
RT expressed neural cell adhesion molecules.";
RL J. Neurosci. 15:2141-2156(1995).
CC -I- FUNCTION: Neural cell adhesion molecule.
CC -I- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -I- TISSUE SPECIFICITY: Central nervous system.

```

```

CC -I- DEVELOPMENTAL STAGE: Expressed at high levels in several
CC developing projection systems: in neurons of the thalamus,
CC subplate, and lower cortical laminae in the forebrain and in the
CC pontine nucleus, cerebellar granule cells, and Purkinje cells in
CC the hindbrain.
CC -I- SIMILARITY: Belongs to the immunoglobulin superfamily. IgION
CC family.
CC -I- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC
CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U16845; AAA67445.1; -.
CC PIR; I56551; I56551.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC Pfam; PF00047; ig; 3.
CC SMART; SM00408; IGC2; 2.
CC PROSITE; PS00835; IG_LIKE; 3.
KW Cell adhesion; Direct protein sequencing; Glycoprotein; GPI-anchor;
KW Immunoglobulin domain; Lipoprotein; Repeat; Signal.
FT SIGNAL 1 33 Potential.
FT CHAIN 34 321 Neurotrophin.
FT PROPEP 322 344 Removed in mature form (Potential).
FT DOMAIN 39 126 Ig-like C2-type 1.
FT DOMAIN 136 218 Ig-like C2-type 2.
FT DOMAIN 222 309 Ig-like C2-type 3.
FT DISULFID 57 115 Potential.
FT DISULFID 157 201 Potential.
FT DISULFID 243 295 Potential.
FT CARBOHYD 44 44 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 70 70 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 152 152 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 216 216 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 284 284 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 292 292 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 305 305 N-linked (GlcNAc... ) (Potential).
FT CARBOHYD 321 321 N-linked (GlcNAc... ) (Potential).
FT LIPID 321 321 GPI-anchor amidated asparagine (Potential).
SQ SEQUENCE 344 AA; 37998 MW; CBB39BE53B3224 CRC64;

Query Match 90.8%; Score 1639.5; DB 1; Length 344;
Best Local Similarity 92.9%; Pred. No. 2.3e-122;
Matches 312; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

QY 12 ISWAIFTGLAALCLF---QGVPRVSGDATFPKAMDNVTVRQGESATLRCITDNRVTRVAV 68
Db 9 LPWKCLVVSLRLFLVPTGVPVRSGDATFPKAMDNVTVRQGESATLRCITDNRVTRVAV 68
QY 69 LNRSTLYAGNDKWCLDPRVLLSNTQYSIEIQNVVDVDEGPTCSVQTDNHPKTSRV 128
Db 69 LNRSTLYAGNDKWCLDPRVLLSNTQYSIEIQNVVDVDEGPTCSVQTDNHPKTSRV 128
QY 129 HLIVQSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEI 188
Db 129 HLIVQSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEI 188
QY 189 QGITREOSGDYECASNDVAAPVRRVKVTNVPYPISEAKGTGVPVGQGTIQCEASAV 248
Db 189 QGITREOSGDYECASNDVAAPVRRVKVTNVPYPISEAKGTGVPVGQGTIQCEASAV 248
QY 249 PSAEFQWKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTASI 308
Db 249 PSAEFQWKDDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTASI 308
QY 309 MLFGPGAVSEVNGTSRRAGCIVLLPLLVHLHLK 344

```

```

Db 309 MLFGPGAVSEVNGTSSRAGCIWLLPLVLHLLKF 344
RESULT 5
CEPU_CHECK
ID CEPU_CHECK STANDARD; PRT; 353 AA.
AC Q90773;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE CEPU-1 protein precursor.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=96370549; PubMed=8774445;
RA Spatmann F., Bruemendorf T.;
RT "CEPU-1, a novel immunoglobulin superfamily molecule, is expressed by
developing cerebellar Purkinje cells.";
RL J. Neurosci. 16:1770-1779(1996).
CC -!- FUNCTION: It may be a cellular address molecule specific to
Purkinje cells. It may represent a receptor or a subunit of a
receptor complex.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=Minor;
CC IsoId=Q90773-1; Sequence=Displayed;
CC Names=2; Synonyms=Major;
CC IsoId=Q90773-2; Sequence=VSP_002607;
CC -!- TISSUE SPECIFICITY: Found on the dendrites, somata and axons of
developing Purkinje cells. Undetectable on other neurons like
Golgi or granule cells.
CC -!- DEVELOPMENTAL STAGE: Expressed by developing cerebellar Purkinje
cells. Expression coincides with the growth of the dendritic tree,
after Purkinje cells have finished their migration from the
ventricular zone (from E15 until E21). Expressed in the adult.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. IgION
family.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-----
This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
-----
DR EMBL; Z72497; CAA96578.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IgC2; 2.
DR PROSITE; PS00835; Ig_LIKE; 3.
KW Alternative splicing; Cell adhesion; Glycoprotein; GPI-anchor;
KW Immunoglobulin domain; Lipoprotein; Repeat; Signal.
FT SIGNAL 1 28
FT CHAIN 29 330
FT PROPEP 331 353
FT DOMAIN 37 124
FT DOMAIN 134 216
FT DOMAIN 220 314
FT DISULFID 55 113
FT DISULFID 155 199
FT DISULFID 241 293
FT CARBOHYD 42 42
FT CARBOHYD 68 68
FT CARBOHYD 150 150

```

Query Match 81.8%; Score 1477.5; DB 1; Length 353;  
Best Local Similarity 78.8%; Pred. No. 2e-109;  
Matches 276; Conservative 32; Mismatches 32; Indels 11; Gaps 1;

QY 5 QPKMHSISWAIETGLAALCLFGQVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRVT 64  
DB 3 QAKQHPVSVWIFAGMAALLFGQVPRSGDATFPKAMDNVTVRQGESATLRCSVDNRVT 62  
QY 65 RVALLNRSTLYAGNDKWCILDPRVLLSNTQTQYSIEIQNVVDVYDEGPTCSVOTDNHPK 124  
DB 63 RVALLNRSSILYAGNDKWCILDPRVLLANTKTQYSIQIHVDVYDEGPTCSVOTDNHPK 122  
QY 125 TSVRLHIVQSPKIVISDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDE 184  
DB 123 TSVRLHIVQSPKITETSSDISINEGNSLTCTATGRPDPTITRRHISPKAVGFISEDE 182  
QY 185 YLEIQGITREQSGDYECSSASNDVAAVPVRRVKVTYVPPYISBAKGTGVPVGKGLTQCE 244  
DB 183 YLEITGITREQSGEYECSSASNDVAAVPVQRVKVTYVPPYISDAKSTGVPVGKGLMCE 242  
QY 245 ASAVPSAEFQWYKDKRLIEGKGVKNRPFUSKLIFFNVSEHDYGNFYTCVSNKLGHT 304  
DB 243 ASAVPSADFWYKDKRLAEGQKLVENKAFPSRLTFFNVSRQDYGNFYTCVASNQLGNT 302  
QY 305 NASIMLPF-----GPGAVSEVNGTSSRAGCIWLLPLVLHLLKF 344  
DB 303 NASMILYEETTTALTTPWKGPGAVHDGNSGAWRRGSCAWLLALPLAQLARQF 353

RESULT 6  
OS7596 PRELIMINARY; PRT; 313 AA.  
ID OS7596; PRELIMINARY; PRT; 313 AA.  
AC OS7596;  
DT 01-JUN-1998 (TrEMBLrel. 06, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Neural secreted glycoprotein (CEPU-Se alpha 2 isoform).  
GN Name=CEPU; Synonyms=CEPU-Se;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99347334; PubMed=10420985;  
RA Kim D.S., Rhew T.H., Moss D.J., Kim J.Y.;  
RT "cDNA cloning of the CEPU, a secreted type of neural glycoprotein  
belonging to the immunoglobulin-like oploid binding cell adhesion  
molecule (OBCAM) subfamily.";  
RL Mol. Cells 9:270-276(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Kim D.;  
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ225897; CAA12649.1; -;  
DR EMBL; AF292935; AAG01878.1; -;  
DR HSSP; Q9UQH9; 1DJS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.

```
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 313 AA; 34482 MW; 99ADB25CAE4A5347 CRC64;

Query Match 79.1%; Score 1428; DB 2; Length 313;
Best Local Similarity 85.4%; Pred. No. 1.5e-105;
Matches 263; Conservative 27; Mismatches 18; Indels 0; Gaps 0;

QY 5 QPKWHSNISWAIFGLTGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRVT 64
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 3 QAKQHPVSVIIFAGMAALLLFGQVPRSGDATFPKAMDNVTVRQGESATLRCSVNRVT 62
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 65 RVAWLNRSILYAGNDKWCCLDPRVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTDNHPK 124
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 63 RVAWLNRSILYAGNDKWCCLDPRVLLANTKTOYSIQIHVDVYDEGPTCSVQTDNHPK 122
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 125 TSRVHLIVQSPKIVEISSDISINEGNNISLTCTATGRPEPTTWRHISP KAVGFVSEDE 184
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 123 TSRVHLIVQSPKITEISSDISINEGNNISLTCTATGRPDPTTWRHISP KAVGFISEDE 182
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 185 YLEITQITRQSGDYECASNDVAAPVVRVKVTVNYPPYISBAKGTGVPVGKGLTQCE 244
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 183 YLEITQITRQSGEYECASNDVAAPVVRVKVTVNYPPYISDAKSTGVPVGKGLMCE 242
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 245 ASAVPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLIGHT 304
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 243 ASAVPSADFQWKDKRLAEGKGLKVENKAFPSRLTFFNVSEQDYGNVTCVASNQLGNT 302
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 305 NASIMLPG 312
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 303 NASMILYG 310
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q93242 ID Q93242 PRELIMINARY; PRT; 344 AA.
AC Q93242;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CEFU-1.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimura Y., Shirabe K., Fukushima M., Takeshita M., Tanaka H.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011810; BAA31514.1; -.
DR HSSP; Q9UQH9; 1DJS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 344 AA; 37613 MW; 22CAA8F526A6B57E CRC64;

Query Match 79.0%; Score 1427.5; DB 2; Length 344;
Best Local Similarity 79.2%; Pred. No. 1.8e-105;
Matches 267; Conservative 31; Mismatches 36; Indels 3; Gaps 1;

QY 11 SISWAIFTGLAALCLF---QGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVA 67
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 8 ALPWRCLVLCRLFLVPAGVPRSGDATFPKAMDNVTVRQGESATLRCSVDNRVTRVA 67
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 68 WLNRSILYAGNDKWCCLDPRVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTDNHPKTSR 127
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 68 WLNRSILYAGNDKWCCLDPRVLLANTKTOYSIQIHVDVYDEGPTCSVQTDNHPKTSR 127
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 128 VHLIVQSPKIVEISSDISINEGNNISLTCTATGRPEPTTWRHISP KAVGFVSEDEYLE 187
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 128 VHLIVQSPKITEISSDISINEGNNISLTCTATGRPDPTTWRHISP KAVGFISEDEYLE 187
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 188 IQGITRQSGDYECASNDVAAPVVRVKVTVNYPPYISBAKGTGVPVGKGLTQCEASA 247
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 188 ITGITRQSGEYECASNDVAAPVVRVKVTVNYPPYISDAKSTGVPVGKGLMCEASA 247
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 248 VPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLIGHTNAS 307
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 248 VPSADFQWKDKRLAEGKGLKVENKAFPSRLTFFNVSEQDYGNVTCVASNQLGNTNAS 307
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 308 IMLFG 312
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 308 MILYG 312
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
Q9DG15 ID Q9DG15 PRELIMINARY; PRT; 315 AA.
AC Q9DG15;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE CEFU-Se alpha 1 isoform.
GN Name=CEFU-Se;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Lodge A.P., McNamee C.J., Howard M.R., Reed J.E., Moss D.J.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF292936; AAG01879.1; -.
DR HSSP; Q9UQH9; 1DJS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003598; IG_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 315 AA; 34606 MW; 68C5D27F0DDC6FB2 CRC64;

Query Match 75.2%; Score 1357.5; DB 2; Length 315;
Best Local Similarity 83.0%; Pred. No. 6.2e-100;
Matches 253; Conservative 26; Mismatches 23; Indels 3; Gaps 1;

QY 11 SISWAIFTGLAALCLF---QGVPRSGDATFPKAMDNVTVRQGESATLRCTIDNRVTRVA 67
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 8 ALPWRCLVLCRLFLVPAGVPRSGDATFPKAMDNVTVRQGESATLRCSVDNRVTRVA 67
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 68 WLNRSILYAGNDKWCCLDPRVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTDNHPKTSR 127
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 68 WLNRSILYAGNDKWCCLDPRVLLANTKTOYSIQIHVDVYDEGPTCSVQTDNHPKTSR 127
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 128 VHLIVQSPKIVEISSDISINEGNNISLTCTATGRPEPTTWRHISP KAVGFVSEDEYLE 187
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 128 VHLIVQSPKITEISSDISINEGNNISLTCTATGRPDPTTWRHISP KAVGFISEDEYLE 187
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 188 IQGITRQSGDYECASNDVAAPVVRVKVTVNYPPYISBAKGTGVPVGKGLTQCEASA 247
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 188 ITGITRQSGEYECASNDVAAPVVRVKVTVNYPPYISDAKSTGVPVGKGLMCEASA 247
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 248 VPSAEFQWKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLIGHTNAS 307
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 248 VPSADFQWKDKRLAEGKGLKVENKAFPSRLTFFNVSEQDYGNVTCVASNQLGNTNAS 307
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 308 IMLFG 312
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 308 MILYG 312
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 9
Q6DFY2 Q6DFY2 PRELIMINARY; PRT; 337 AA.
AC Q6DFY2
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein 3732419F12.
GN Name=3732419F12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
RA Director MGC Project;
RA Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC076581; AAH76581.1;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS50835; IG LIKE; 3.
KW Hypothetical protein_
SQ SEQUENCE 337 AA; 37156 MW; 2A279D982E60F4AB CRC64;

Query Match 72.3%; Score 1306; DB 2; Length 337;
Best Local Similarity 72.1%; Pred. No. 8.6e-96;
Matches 243; Conservative 35; Mismatches 59; Indels 0; Gaps 0;

QY 8 MHSISWAIETGLAALCLFQGVPRSGDATFPKAMDNVTVRQGESATLRCITIDRVTVA 67
DB 1 MYHPAYWIVFSATALLFIPGVPRSGDATFPKAMDNVTVRQGESATLRCITIDRVTVA 60
QY 68 WLNKRSTLYAGNDKWCILDPRVLLSNTQCYSTQYEQNVVDYDRGPTCSVQTDNHPKTSR 127
DB 61 WLNKRSTLYAGNDKWDSDPRVILVNTPTQYSIMIQNDVDYDRGPTCSVQTDNHPKTSR 120
QY 128 VHLIVQSPKIVRISDISINEGNISLTCATCRPEPTVTRHISPKAVGFVSEDEYLE 187
DB 121 VHLIVQVPPQIMNISSDITVNEGSSVLLCLAIGRPEPTVTRHLSVKGGFVSEDEYLE 180
QY 188 IQGITREQSGDYECASNDVAAPVRRVKVTVYPPYISAKGTGVPVQKGTLQCEASA 247
DB 181 ISDKRQDSGEYECASALNDVAAPVRRVKVTVYPPYISAKNTGVSQVKGTLQCEASA 240

248 VPSAEFOWYKDKRLTEGKGVKVENRPFLSKLIFFNVSBHDYGNVTCVASNKLGHNTAS 307
241 VPMAEFOWFKEDTRLATGLDGVRIENKGRISTLTFFNVSEKDYGNVTCVAINKLGNNTAS 300
308 IMIFGPGAVSEVNGTSRRRAGCVWLPLPLVLLHLLKF 344
301 ITLYGPGAVIDGVNSASRALACLWLSGTFFFAHFFIKF 337

RESULT 10
OPCM CHICK
ID OPCM_CHICK STANDARD; PRT; 337 AA.
AC Q98892;
DT 01-NOV-1997 (Rel. 35, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Opioid binding protein/cell adhesion molecule homolog precursor
DE (Neurite inhibitor GP55-A) (OBCAM protein gamma isoform).
GN Name=OPCML;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
SEQUENCE FROM N.A.
TISSUE=Brain;
RA Lodge A.P., Kim D.-S., Howard M.R., McNamee C.J., Smith N., Moss D.J.;
RT "Cloning of CEPU-S, a secreted isoform of CEPU-1, and OBCAM cDNAs from
RT chick: structural diversity of IGLON family proteins."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE OF 64-337 FROM N.A., AND PARTIAL SEQUENCE.
TISSUE=Brain;
RX MEDLINE=97157768; PubMed=9004047;
RA Wilson D.J.A., Kim D.-S., Clarke G.A., Marshall-Clarke S., Moss D.J.;
RT "A family of glycoproteins (GP55), which inhibit neurite outgrowth,
RT are members of the Ig superfamily and are related to OBCAM,
RT neurotrophin, LAMP and CEPU-1."
RL J. Cell Sci. 109:3129-3138(1996).
CC -I- FUNCTION: Inhibits neurite outgrowth.
CC -I- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -I- TISSUE SPECIFICITY: Restricted to the nervous system.
CC -I- DEVELOPMENTAL STAGE: Increases during development from very low
CC levels at embryonic day 10 and is most abundant after hatching.
CC -I- SIMILARITY: Belongs to the immunoglobulin superfamily. IGLON
CC family.
CC -I- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; Y08170; CAB41420.1; -.
CC HSSP; P78310; 1F5W.
CC InterPro; IPR007110; Ig-like.
CC Pfam; PF00047; Ig; 3.
CC PROSITE; PS50835; IG LIKE; 3.
CC Cell adhesion; Direct protein sequencing; Glycoprotein; GPI-anchor;
CC Immunoglobulin domain; Lipoprotein; Membrane; Repeat; Signal.
FT SIGNAL 1 20 By similarity.
FT CHAIN 21 314 Opioid binding protein/cell adhesion
FT molecule homolog.
FT PROPEP 315 337 Removed in mature form (Potential).
FT DOMAIN 32 119 Ig-like C2-type 1.
FT DOMAIN 129 211 Ig-like C2-type 2.
FT DOMAIN 215 302 Ig-like C2-type 3.
FT DISULFID 50 108 Potential.
FT DISULFID 150 194 Potential.
```



FT	DISULFID	236	288	Potential.	
FT	LIPID	314	314	GPI-anchor amidated asparagine (Potential).	
FT	CARBOHYD	133	133	N-linked (GlcNAc. . .) (Potential).	
FT	CARBOHYD	277	277	N-linked (GlcNAc. . .) (Potential).	
FT	CARBOHYD	285	285	N-linked (GlcNAc. . .) (Potential).	
FT	CARBOHYD	298	298	N-linked (GlcNAc. . .) (Potential).	
SQ	SEQUENCE	337 AA; 36887 MW;	BAE717551856651E CRC64;		
Query Match					
Best Local Similarity 73.2%; Score 1305; DB 1; Length 337;					
Matches 248; Conservative 34; Mismatches 53; Indels 4; Gaps 2;					
QY	8	MNNSISWAIPTGLAALCLFQGVPRSGDATFPKAMDNTVTRQGESATLRCTIDNRVTRVA	67		
Db	1	MYHPACWIVFTATTALLFIPGVPRSGDATFPKAMDNTVTRQGESATLRCTVDDRVRVA	60		
QY	68	WLNRSITLYAGNDKWCLDPRVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTDNHPKTSR	127		
Db	61	WLNRSITLYAGNDKWSIDNRVILSNTKTQYSIKIHNVVDYDEGPTCSVQTDNHPKTSR	120		
QY	128	VHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFVSEDEYLE	187		
Db	121	VHLIVQVPPQIWNISDITVNEGSSVTLMCFLAAGRPEPTVTRHLSKGQGFVSEDEYLE	180		
QY	188	IQGITREOSGDYECASNDVAAPVRRVKVTNYPPISEAKGTGVPVGOKGTLOCEASA	247		
Db	181	ITGITREOSGEYECASNDVAAPDVRKVKTNYPPISEAKNTGASVGOKGILQCEASA	240		
QY	248	VPSAEFQWKDKRLIEGKGVKVENRPFSLKIFNVSEHDYGNVTCVASNKLGHNTAS	307		
Db	241	VPVAEFQWFKEDTRLANGLEGVRIEKGRLSTLTFNVSEKDYGNVTCVATNKLGNNTAS	300		
QY	308	IMLFGGAVSEVSGTSRRAG--CVWLLPLLVLLHLKLF	344		
Db	301	IILYGCAVHDSGNAASRAAGLCLW--ATLLARLLLDLF	337		
RESULT 11					
ID	Q723W6	PRELIMINARY;		PRT;	338 AA.
AC	Q723W6;				
DT	01-OCT-2003	(T-EMBLrel. 25, Created)			
DT	01-OCT-2003	(T-EMBLrel. 25, Last sequence update)			
DE	Hypothetical protein DKF2p686H1949.				
GN	Names=DKF2p686H1949;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Human amygdala;				
RA	Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;				
RL	Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BX537377; CAD97619.1; -				
DR	HSSP; Q9UQH9; 1IIL.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003598; Ig_c2.				
DR	Pfam; PF00047; ig; 2.				
DR	SMART; SM00408; IGC2; 2.				
DR	PROSITE; PS50835; IG_LIKE; 3.				
KW	Hypothetical protein.				
SQ	SEQUENCE 338 AA; 37267 MW; EDD86EE2C57B09E3 CRC64;				
Query Match					
Best Local Similarity 71.6%; Score 1295.5; DB 2; Length 338;					
Matches 242; Conservative 38; Mismatches 57; Indels 1; Gaps 1;					
QY	8	MNNSISWAIPTGLAALCLFQGVPRSGDATFPKAMDNTVTRQGESATLRCTIDNRVTRVA	67		
Db	1	MYHPACWIVFTATTALLFIPGVPRSGDATFPKAMDNTVTRQGESATLRCTVDDRVRVA	60		
QY	68	WLNRSITLYAGNDKWCLDPRVLLSNTQTOYSIEIQNVVDYDEGPTCSVQTDNHPKTSR	127		
Db	61	WLNRSITLYAGNDKWSIDNRVILSNTKTQYSIKIHNVVDYDEGPTCSVQTDNHPKTSR	120		
QY	128	VHLIVQSPKIVEISSDISINEGNNISLTCIATGRPEPTVTRHISPKAVGFVSEDEYLE	187		
Db	121	VHLIVQVPPQIWNISDITVNEGSSVTLMCFLAAGRPEPTVTRHLSKGQGFVSEDEYLE	180		
QY	188	IQGITREOSGDYECASNDVAAPVRRVKVTNYPPISEAKGTGVPVGOKGTLOCEASA	247		
Db	181	ITGITREOSGEYECASNDVAAPDVRKVKTNYPPISEAKNTGASVGOKGILQCEASA	240		
QY	248	VPSAEFQWKDKRLIEGKGVKVENRPFSLKIFNVSEHDYGNVTCVASNKLGHNTAS	307		
Db	241	VPVAEFQWFKEDTRLANGLEGVRIEKGRLSTLTFNVSEKDYGNVTCVATNKLGNNTAS	300		
QY	308	IMLFGGAVSEVSGTSRRAG--CVWLLPLLVLLHLKLF	344		
Db	301	IILYGCAVHDSGNAASRAAGLCLW--ATLLARLLLDLF	337		



RA Klein S., Gerhard D.S.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC074283; AAH74283.1; --  
DR InterPro; IPR003599; Ig-like.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00409; Ig; 3.  
DR SMART; SM00408; IGC2; 3.  
DR SMART; SM00406; IGV; 2.  
DR PROSITE; PS50835; IG-LIKE; 3.  
SQ SEQUENCE 345 AA; 38166 MW; C2BE84F5A2EECA6 CRC64;

Query Match 70.7%; Score 1276.5; DB 2; Length 345;  
Best Local Similarity 71.7%; Pred. No. 2e-93;  
Matches 243; Conservative 43; Mismatches 44; Indels 9; Gaps 2;

QY 12 ISWAIFTGLAALCLF-----QGVPRSGDATFPKAMDNVTVRQGESATLRCITIDNRVTR 65  
DB 1 MGFAPWRWLLALCLRLFLVPAGVPRSGDAGFPKAMDNVTVRQGSAILRCTVDNRVTR 60  
QY 66 VAWLNRSITLYAGNDKWLDRVLLSNTQTSYIEIQNVVDYDEGPTCSVQTDNHPKT 125  
DB 61 VAWLNRSITLYTGNDKWSIDPRVLLANTKSYIEIQNVVDYDEGPTCSVQTDNHPKT 120  
QY 126 SRVHLIVQVSPKIVEISSDINSGNISLTCTATGPEPTVTRHISPKAVGFVSEDEY 185  
DB 121 SRVHLIVQVPRVIDISNTAVNGSNVSLCTATGPEPTVTRHISPKAVGFVSEDEY 180  
QY 186 LEIQITRQSGDYECASNDVAAPVVRVKVTNNPPYIIEAKGTGVPVQKGTLCQEA 245  
DB 181 LEIQITRQSGDYECASNDVSDAPVRRVKLTNNPPYIIEAKGTGVPVQKGTLCQEA 240  
QY 246 SAVPSAEFQYKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGYNTCVASNKLGHNT 305  
DB 241 SAVPAADFQYKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGYNTCVASNKLGHNT 300  
QY 306 ASIMLFGPGAVSEVSGTSTRAG--CVWLLPLLVLLHLKLF 344  
DB 301 ASIMLFGPGAVHDGNSGSPQ---CPFCAPLLELLLELL 336

## RESULT 13

ID Q9DF61 PRELIMINARY; PRT; 344 AA.  
AC Q9DF61  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE OBCAM alpha 1 isoform.  
GN Name=OBCAM;  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20499204; PubMed=11042360; DOI=10.1016/S0169-328X(00)00184-4;  
RA Lodge A.P., Howard M.R., McNamee C.J., Moss D.J.;  
RT "Co-localisation, heterophilic interactions and regulated expression  
of IgLON family proteins in the chick nervous system.";  
RL Brain Res. Mol. Brain Res. 82:84-94 (2000).  
DR HSSP; P13596; IQZ1.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003598; Ig\_c2.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00408; IGC2; 2.  
DR PROSITE; PS50835; IG-LIKE; 3.  
SQ SEQUENCE 344 AA; 37530 MW; 37F86051CBF0E7B4 CRC64;

Query Match 70.6%; Score 1275.5; DB 2; Length 344;  
Best Local Similarity 72.8%; Pred. No. 2.4e-93;  
Matches 246; Conservative 32; Mismatches 53; Indels 7; Gaps 3;

QY 12 ISWAIFTGLAALCLF---QGVPRSGDATFPKAMDNVTVRQGESATLRCITIDNRVTRVAV 68  
DB 9 LPWRCLVVLCLRLFLVPAGVPRSGDAGFPKAMDNVTVRQGESATLRCITVDRVRVAV 68  
QY 69 LNRSTILYAGNDKWLDRVLLSNTQTSYIEIQNVVDYDEGPTCSVQTDNHPKTSRV 128  
DB 69 LNRSTILYAGNDKWSIDNRVILSNTQTSYIEIQNVVDYDEGPTCSVQTDNHPKTSRV 128  
QY 129 HLIVQVSPKIVEISSDINSGNISLTCTATGPEPTVTRHISPKAVGFVSEDEYLEI 188  
DB 129 HLIVQVPPQVILNSSLITVNEGSSVILMCLAFGRPEPTVTRHLSGKQGFVSEDEYLEI 188  
QY 189 QGITRQSGDYECASNDVAAPVVRVKVTNNPPYIIEAKGTGVPVQKGTLCQEAASV 248  
DB 189 TGITRQSGDYECASNDVAVPDRVKVTNNPPYIISNAKNTGASVGQKGLQEAASV 248  
QY 249 PSAEFQYKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGYNTCVASNKLGHNTASI 308  
DB 249 PVAEFQYKDKRLIEGKGVKVENRPFSLKLIFFNVSEHDYGYNTCVATNKLGNASI 308  
QY 309 MLFGPGAVSEVSGTSTRAG--CVWLLPLLVLLHLKLF 344  
DB 309 ILYGPAGVHDGNSGAARAAAGLCIM--ATLLARLLLD 344

## RESULT 14

ID Q6B014 PRELIMINARY; PRT; 344 AA.  
AC Q6B014  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Opioid-binding cell adhesion molecule.  
GN Name=OPCML;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RP SEQUENCE FROM N.A.  
RC TISSUE=Fetal Brain;  
RA Director MGC Project;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC074742; AAH74742.1; --

```
DR InterPro; IPR003599; Ig_c2.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 3.
DR SMART; SM00408; IGC2; 3.
DR PROSITE; PS00835; IG LIKE; 3.
SQ SEQUENCE 344 AA; 37868 MW; 15BPE574797B15F3 CRC64;

Query Match 70.3%; Score 1270.5; DB 2; Length 344;
Best Local Similarity 71.1%; Pred. No. 6e-93;
Matches 239; Conservative 37; Mismatches 57; Indels 3; Gaps 1;

Qy 12 ISWAIFGLAALCLF---QGVPRVSGDATPKAMDNVTVRQGESATLRCITDNRVTVAV 68
Db 9 LPWKCLVVSRLFLVPTGVPVSGDATPKAMDNVTVRQGESATLRCITDNRVTVAV 68
Qy 69 LNRSTILYAGNDKWLCDPRVLLSNTQTSIEIQNVVDVDEGPTCSVQTDNHPKTSRV 128
Db 69 LNRSTILYAGNDKWSIDPRVILVNTPTQYSIMIQNVVDVDEGPTCSVQTDNHPKTSRV 128
Qy 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEI 188
Db 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEI 188
Qy 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEI 188
Db 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEI 188
Qy 189 QGITRQSGDYECASNDVAAPVRRVKVTVNPPYISEAKGTGVPVQKGTLQCEASAV 248
Db 189 SDIKRQSGDYECASNDVAAPVRRVKVTVNPPYISEAKGTGVPVQKGTLQCEASAV 248
Qy 249 PSAEFQWKDKRLIEGKGVKVNRPPLSKLIFPNVSEHDYGYNTCVASNKLGHNTASI 308
Db 249 PSAEFQWKDKRLIEGKGVKVNRPPLSKLIFPNVSEHDYGYNTCVASNKLGHNTASI 308
Qy 309 MLFQPGAVSEVNGTSRRAGCVLLPLVLLHLLKF 344
Db 309 TLYGPGAVIDGVNSASRALACLWLSGTLAHFFIKF 344

RESULT 15
OPCM HUMAN
ID OPCM HUMAN STANDARD; PRT; 345 AA.
AC Q14982;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Opioid binding protein/cell adhesion molecule precursor (OB CAM)
DE (Opioid-binding cell adhesion molecule) (OPCML).
GN Name=OPCML; Synonyms=OB CAM;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Occipital cortex;
RX MEDLINE=95237612; PubMed=7721093; DOI=10.1016/0378-1119(94)00830-L;
RA Shark K.B.; Lee N.M.;
RT "Cloning, sequencing and localization to chromosome 11 of a cDNA
RL encoding a human opioid-binding cell adhesion molecule (OB CAM).";
RL Gene 155:213-217(1995).
CC -1- FUNCTION: Binds opioids in the presence of acidic lipids; probably
CC involved in cell contact.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC similarity).
CC -1- SIMILARITY: Belongs to the immunoglobulin superfamily. IgLON
CC family.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
```

```
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; L34774; AAA36387.1; -.
CC PIR; JC4025; JC4025.
CC Genew; HGNC:8143; OPCML.
CC MIM; 60632; -.
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0004985; F:opioid receptor activity; TAS.
CC GO; GO:0007155; P:cell adhesion; TAS.
CC GO; GO:0008038; P:neuronal cell recognition; TAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00408; IGC2; 2.
CC PROSITE; PS00835; IG LIKE; 3.
CC Cell adhesion; Glycoprotein; GPI-anchor; Immunoglobulin domain;
KW Lipoprotein; Repeat; Signal.
FT SIGNAL 1
FT CHAIN 28 322
FT PROPEP 323 345
FT DOMAIN 39 126
FT DOMAIN 136 219
FT DOMAIN 223 310
FT DISULFID 57 115
FT DISULFID 157 202
FT DISULFID 244 296
FT CARBOHYD 44 44
FT CARBOHYD 70 70
FT CARBOHYD 140 140
FT CARBOHYD 285 285
FT CARBOHYD 293 293
FT CARBOHYD 306 306
FT CARBOHYD 322 322
FT LIPID 322 322
FT SEQUENCE 345 AA; 38007 MW; E7AD17BEA1AA3FF4 CRC64;

Query Match 70.2%; Score 1268; DB 1; Length 345;
Best Local Similarity 71.2%; Pred. No. 9.5e-93;
Matches 240; Conservative 37; Mismatches 56; Indels 4; Gaps 2;

Qy 12 ISWAIFGLAALCLF---QGVPRVSGDATPKAMDNVTVRQGESATLRCITDNRVTVAV 68
Db 9 LPWKCLVVSRLFLVPTGVPVSGDATPKAMDNVTVRQGESATLRCITDNRVTVAV 68
Qy 69 LNRSTILYAGNDKWLCDPRVLLSNTQTSIEIQNVVDVDEGPTCSVQTDNHPKTSRV 128
Db 69 LNRSTILYAGNDKWSIDPRVILVNTPTQYSIMIQNVVDVDEGPTCSVQTDNHPKTSRV 128
Qy 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEI 187
Db 129 HLIVQVSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEI 187
Qy 188 IQGITRQSGDYECASNDVAAPVRRVKVTVNPPYISEAKGTGVPVQKGTLQCEASA 247
Db 188 IQGITRQSGDYECASNDVAAPVRRVKVTVNPPYISEAKGTGVPVQKGTLQCEASA 247
Qy 189 ISDIKRDQSGDYECASNDVAAPVRRVKVTVNPPYISEAKGTGVPVQKGTLQCEASA 248
Db 189 ISDIKRDQSGDYECASNDVAAPVRRVKVTVNPPYISEAKGTGVPVQKGTLQCEASA 248
Qy 248 VPSAEFQWKDKRLIEGKGVKVNRPPLSKLIFPNVSEHDYGYNTCVASNKLGHNTASI 307
Db 248 VPSAEFQWKDKRLIEGKGVKVNRPPLSKLIFPNVSEHDYGYNTCVASNKLGHNTASI 307
Qy 249 VPSAEFQWKDKRLIEGKGVKVNRPPLSKLIFPNVSEHDYGYNTCVATNKLGNINAS 308
Db 249 VPSAEFQWKDKRLIEGKGVKVNRPPLSKLIFPNVSEHDYGYNTCVATNKLGNINAS 308
Qy 308 IMLFQPGAVSEVNGTSRRAGCVLLPLVLLHLLKF 344
Db 308 IMLFQPGAVSEVNGTSRRAGCVLLPLVLLHLLKF 344
Qy 309 ITLYGPGAVIDGVNSASRALACLWLSGTLAHFFIKF 345
Db 309 ITLYGPGAVIDGVNSASRALACLWLSGTLAHFFIKF 345
```

Search completed: October 19, 2005, 16:32:03  
Job time : 203 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 19, 2005, 16:27:21 ; Search time 41 Seconds  
(without alignments)

807.282 Million cell updates/sec

Title: US-09-978-544A-523

Perfect score: 1806

Sequence: 1 MKTIQPKMHSISWAIFTGL.....RRAGCVMLPLVLHLLKKF 344

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1500 summaries

Database :

PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1639.5	90.8	344	2	I56551
2	1285.5	71.2	338	2	JC1238
3	1268	70.2	345	2	JC4025
4	1266	70.1	345	2	S03199
5	1259	69.7	345	2	JC1239
6	936.5	51.9	338	2	JC5519
7	931.5	51.6	338	2	JC4776
8	297.5	16.5	333	2	A31923
9	283.5	15.7	725	1	IJMSNG
10	283.5	15.7	1115	1	IJMSNL
11	279.5	15.5	725	2	IJC099
12	279.5	15.5	1091	1	IJC099
13	278.5	15.4	4162	2	T42633
14	277.5	15.4	858	1	IJRTNC
15	277.5	15.4	1088	1	IJXLNL
16	276	15.3	761	1	IJC099
17	275.5	15.3	853	1	IJC099
18	273.5	15.1	725	2	JN0568
19	272.5	15.1	1323	2	JN0568
20	270.5	15.0	1092	1	JN0568
21	261.5	14.5	1091	2	S01998
22	259	14.3	7962	2	I38346
23	254.5	14.1	5175	2	T20992
24	254.5	14.1	5198	2	T43290
25	249.5	13.8	1040	2	A49356
26	246.5	13.6	1018	2	A54744
27	243.5	13.5	1021	2	A57112
28	243.5	13.5	1036	2	S22383
29	241.5	13.4	1018	2	JC4211

neuronal cell surf  
heparan sulfate pr  
hypothetical prote  
axonal glycoprotei  
hypothetical prote  
CD22 homolog/B lym  
kinase-like protei  
protein UNC-89 - C  
paracrine precursor  
differentiation an  
Down syndrome cell  
fasciclin II precu  
glial cell membran  
dutt1 protein - mo  
neuroglial - fruit  
protein-tyrosine k  
transmembrane rece  
hypothetical prote  
fasciclin II, tran  
fasciclin II pi-li  
plasmacytoma-associ  
BIG-1 protein - ra  
neogenin - chicken  
eas-3 protein - Ca  
ror-related recept  
nephlin - human  
B-cell adhesion pr  
tumor suppressor p  
hypothetical prote  
myosin-light-chain  
neurofascin - chic  
frazzled gene prot  
frazzled gene prot  
neural cell adhesi  
protein-tyrosine-p  
probable neural ce  
neural cell adhesi  
neural cell adhesi  
CDO protein - rat  
cell adhesion mole  
cell adhesion mole  
cell adhesion mole  
neural cell adhesi  
neural cell adhesi  
hypothetical prote  
CDO protein - huma  
advanced glycosyla  
carcinoembryonic a  
rig-1 protein - mo  
tumor suppressor -  
myelin-associated  
myelin-associated  
cell adhesion prot  
neural cell adhesi  
neural cell adhesi  
hypothetical prote  
Fit-1 tyrosine kin  
myelin-associated  
neural cell adhesi  
receptor tyrosine  
myelin-associated  
telencephalin prec  
hypothetical prote  
Bravo/Nr-CAM cell  
fibroblast growth  
hypothetical prote  
KIAA0992 protein -  
hypothetical prote  
projectin - fruit  
titin, cardiac mus

103	173.5	9.6	1021	2	T42634	connectin/titin -	176	151	8.4	976	1	TVMSMD	macrophage colony-
104	172.5	9.6	264	2	T26976	hypothetical prote	177	151	8.4	1287	2	T30988	hypothetical prote
105	176.5	9.6	976	2	T29583	hypothetical prote	178	150.5	8.3	349	2	A34815	carcinoembryonic a
106	172.5	9.6	1880	2	T18531	tractin - medicina	179	150.5	8.3	824	2	S24108	protein-tyrosine k
107	172	9.5	286	2	A28333	carcinoembryonic a	180	150.5	8.3	1298	2	A48999	protein-tyrosine k
108	172	9.5	647	2	A35648	B-cell adhesion pr	181	150	8.3	769	2	S16236	fibroblast growth
109	171.5	9.5	1338	2	S09982	protein-tyrosine k	182	150	8.3	822	2	A45081	fibroblast growth
110	171	9.5	464	2	C30127	transmembrane carc	183	150	8.3	822	2	A41794	keratinocyte growt
111	171	9.5	526	1	A32164	billary glycoprote	184	149.5	8.3	739	2	JS0675	vascular cell adhe
112	171	9.5	1257	1	A41060	neural cell adhesi	185	149.5	8.3	1501	2	IS8148	protein-tyrosine-p
113	170	9.4	812	1	A36477	fibroblast growth	186	149.5	8.3	1863	2	S46217	protein-tyrosine-p
114	169	9.4	764	2	A49448	irregular chiasm C	187	149	8.3	335	2	H43354	pregnancy-specific
115	169	9.4	814	2	A39752	fibroblast growth	188	149	8.3	1894	2	CS4689	protein-tyrosine-p
116	168	9.3	1330	2	S49010	embryonic receptor	189	148.5	8.2	587	2	JH0464	DM-GRASP precursor
117	168	9.3	2051	2	T30938	receptor tyrosine	190	148.5	8.2	588	2	JH0506	adhesion molecule
118	168	9.3	2295	2	C88369	protein unc-52 [im	191	148.5	8.2	1907	2	SJ0893	protein-tyrosine-p
119	167.5	9.3	523	2	S50478	neurolin - goldfis	192	147.5	8.2	876	2	I49152	protein-tyrosine k
120	167.5	9.3	1694	2	S50065	sialoadhesin - mou	193	147.5	8.2	1499	2	IS0212	protein-tyrosine-p
121	167	9.2	816	2	A49151	fibroblast growth	194	147	8.1	402	2	T09062	probable advanced
122	167	9.2	822	1	TVMSFG	fibroblast growth	195	147	8.1	406	2	E43354	pregnancy-specific
123	167	9.2	1356	2	JC1402	protein-tyrosine k	196	146.5	8.1	773	2	T46283	hypothetical prote
124	165.5	9.2	538	2	JC2457	vascular cell adhe	197	146	8.1	428	2	A27658	pregnancy-specific
125	165.5	9.2	646	2	I38049	cell surface glyco	198	146	8.1	852	2	IS1259	tyrosine kinase C
126	165	9.1	584	2	T08678	hypothetical prote	199	146	8.1	1088	1	PRRTGA	platelet-derived g
127	165	9.1	822	2	I49289	fibroblast growth	200	146	8.1	1089	1	SJ3727	platelet-derived g
128	165	9.1	822	2	S29840	fibroblast growth	201	145.5	8.1	739	2	JN0581	vascular cell adhe
129	165	9.1	2222	2	T13924	sdk protein - fru	202	145.5	8.1	799	2	S18209	fibroblast growth
130	164.5	9.1	583	2	I39428	alcam - human	203	145.5	8.1	1898	2	S46216	leukocyte antigen-
131	164.5	9.1	832	2	JH0393	fibroblast growth	204	145	8.0	972	1	TVHUMD	macrophage colony-
132	164	9.1	628	2	I38000	Lutheran blood gro	205	144.5	8.0	1262	1	B48758	protein-tyrosine-p
133	163	9.0	818	2	T19120	hypothetical prote	206	144.5	8.0	1496	1	A48758	protein-tyrosine-p
134	162.5	9.0	1535	2	S46224	peroxidasin - fru	207	143.5	7.9	1177	2	T16594	hypothetical prote
135	162	9.0	321	2	JH0395	billary glycoprote	208	143.5	7.9	13055	2	T16580	hypothetical prote
136	162	9.0	351	2	JH0396	billary glycoprote	209	143	7.9	620	2	JH0593	Schwann cell myeli
137	162	9.0	417	2	JH0394	billary glycoprote	210	143	7.9	687	2	A49636	soluble vascular e
138	161	8.9	588	2	I37202	B-CAM protein - hu	211	143	7.9	1011	2	T13669	neuromusculin - fr
139	161	8.9	2541	2	T29340	hypothetical prote	212	142.5	7.9	326	2	F43354	pregnancy-specific
140	160.5	8.9	980	1	TVCTMD	macrophage colony-	213	142.5	7.9	435	2	D33258	pregnancy-specific
141	160	8.9	662	2	A40862	heparin-binding gr	214	142.5	7.9	739	2	A41288	vascular cell adhe
142	160	8.9	822	1	TVHUGF	fibroblast growth	215	142	7.9	806	2	A35963	protein-tyrosine k
143	160	8.9	1437	2	T31093	probable protein-t	216	141.5	7.8	324	2	G43354	pregnancy-specific
144	160	8.9	6831	2	A88853	protein unc-22 [im	217	141.5	7.8	333	2	A43354	pregnancy-specific
145	160	8.9	6839	2	S57242	twitchin [similari	218	141.5	7.8	789	2	T28714	hypothetical prote
146	158.5	8.8	1199	2	T32005	hypothetical prote	219	141.5	7.8	1227	2	T23004	hypothetical prote
147	158	8.7	361	2	PN0200	fibroblast growth	220	141.5	7.8	1355	2	T28715	hypothetical prote
148	158	8.7	822	2	B54846	fibroblast growth	221	141	7.8	254	2	C42691	fibroblast growth
149	157.5	8.7	941	1	TVMWVD	protein-tyrosine k	222	141	7.8	821	1	TVHUF2	fibroblast growth
150	157	8.7	299	2	S56749	junctional adhesio	223	140.5	7.8	397	2	C43354	pregnancy-specific
151	156.5	8.7	416	1	A42879	advanced glycosyla	224	140.5	7.8	705	2	S51635	fibroblast growth
152	156	8.6	978	2	S16385	macrophage colony-	225	140.5	7.8	823	2	B35963	protein-tyrosine k
153	155.5	8.6	7160	2	T27935	hypothetical prote	226	140.5	7.8	1089	1	PFHUGA	platelet-derived g
154	155.5	8.6	880	2	B53743	protein-tyrosine k	227	140	7.8	800	1	TVHUF2	fibroblast growth
155	155.5	8.6	1138	2	S24614	myosin-binding pro	228	140	7.8	800	2	A48991	heparin-binding gr
156	155	8.6	458	1	WMMSR1	billary glycoprote	229	140	7.8	801	2	IS5363	protein-tyrosine k
157	155	8.6	458	2	JC1509	billary glycoprote	230	140	7.8	890	1	AS3743	protein-tyrosine k
158	155	8.6	521	2	JC1508	billary glycoprote	231	140	7.8	976	1	TVHUKT	protein-tyrosine k
159	155	8.6	521	2	S34338	billary glycoprote	232	139.5	7.7	395	2	D43354	pregnancy-specific
160	155	8.6	1363	2	I58375	protein-tyrosine k	233	139.5	7.7	417	2	A28277	pregnancy-specific
161	155	8.6	1367	2	A41228	protein-tyrosine k	234	139.5	7.7	419	2	A33258	pregnancy-specific
162	154.5	8.6	602	2	A45769	acetylcholine rece	235	139.5	7.7	419	2	A31135	pregnancy-specific
163	154.5	8.6	1897	1	TDHULK	leukocyte antigen-	236	139.5	7.7	426	2	A35964	pregnancy-specific
164	154	8.5	1348	2	S51656	vascular endotheli	237	139.5	7.7	821	1	TVMSBK	fibroblast growth
165	153.5	8.5	588	2	A45254	surface glycoprote	238	139.5	7.7	1052	2	B49120	protein-tyrosine k
166	153	8.5	1912	2	A56178	protein-tyrosine-p	239	139	7.7	824	2	S36439	fibroblast growth
167	152.5	8.4	267	2	A38442	probable tumor sup	240	139	7.7	987	2	A88746	protein C10R3.2 [i
168	152.5	8.4	458	2	S23969	cell-adhesion mole	241	139	7.7	3488	2	T34418	hypothetical prote
169	152	8.4	525	1	A58674	neurotrophin-3 rec	242	138.5	7.7	413	2	S65948	hemolin - cecropia
170	152	8.4	803	1	S35895	neurotrophin-3 rec	243	138.5	7.7	426	2	B33258	pregnancy-specific
171	152	8.4	819	1	TVCHFG	fibroblast growth	244	138.5	7.7	426	2	A53341	platelet-derived g
172	152	8.4	880	1	JC4166	protein-tyrosine k	245	138	7.6	1087	2	IS1552	platelet-derived g
173	152	8.4	1123	2	S36846	myosin-binding pro	246	137.5	7.6	419	2	B54312	pregnancy-specific
174	151.5	8.4	344	2	A27681	nonspecific cross-	247	137.5	7.6	882	2	I38912	receptor tyrosine
175	151.5	8.4	422	2	S32357	glial growth facto	248	137.5	7.6	1379	2	JC4954	vascular endotheli

249	137	7.6	282	2	C28928	pregnancy-specific	322	124	6.9	436	2	B55181	pregnancy-specific
250	137	7.6	424	2	B36109	pregnancy-specific	323	124	6.9	495	2	A55181	pregnancy-specific
251	137	7.6	458	2	S68177	C-CAM2a protein is	324	124	6.9	650	1	JC1450	fibroblast growth
252	137	7.6	519	2	A44783	ecto-Afrase precu	325	124	6.9	999	2	I38547	novel cellular pro
253	137	7.6	524	2	S35341	ketatin - fruit fly	326	124	6.9	1666	2	A48594	skelamin - mouse
254	136.5	7.6	738	2	A40096	platelet-endotheli	327	123.5	6.8	402	2	A54312	pregnancy-specific
255	136.5	7.6	822	2	S19947	fibroblast growth	328	123.5	6.8	640	2	A43273	heregulin precursor
256	135.5	7.5	822	2	B49151	fibroblast growth	329	123	6.8	351	2	B34595	pregnancy-specific
257	135.5	7.5	975	2	JC30816	macrophage colony-	330	123	6.8	476	1	A35104	brain-derived neur
258	134.5	7.4	419	2	JC4123	pregnancy-specific	331	123	6.8	821	1	S06943	brain-derived neur
259	134.5	7.4	428	2	I57486	pregnancy-specific	332	123	6.8	1176	2	JN0583	myosin-light-chain
260	134.5	7.4	428	2	JS00032	pregnancy-specific	333	122.5	6.8	230	2	A56210	neu differentiatio
261	134.5	7.4	480	2	A56182	fibroblast growth	334	122.5	6.8	241	2	D43273	heregulin precursor
262	134.5	7.4	647	2	B41288	vascular cell adhe	335	122.5	6.8	462	2	I38404	neu differentiatio
263	134.5	7.4	729	2	A49120	fibroblast growth	336	122.5	6.8	636	2	I61718	neu differentiatio
264	134	7.4	238	2	T22098	hypothetical prote	337	122.5	6.8	637	2	C43273	heregulin precursor
265	134	7.4	424	2	A34595	pregnancy-specific	338	122.5	6.8	639	2	I61719	neu differentiatio
266	134	7.4	1147	2	A59307	myosin-light-chain	339	122.5	6.8	645	2	B43273	heregulin, splice
267	133.5	7.4	888	2	S23065	ufo protein - mous	340	122.5	6.8	662	2	I61722	neu differentiatio
268	133	7.4	336	2	C27658	pregnancy-specific	341	122	6.8	272	2	I48268	biliary glycoprote
269	133	7.4	413	2	A37778	hemolin precursor	342	122	6.8	850	2	JC5700	Erbb kinase activa
270	133	7.4	473	2	D88976	protein F5482.4 [i	343	121.5	6.7	332	2	JN0067	pregnancy-specific
271	133	7.4	612	2	I73633	gene trkC protein	344	121.5	6.7	365	2	JC7780	coxsackie- and ade
272	133	7.4	818	2	JC4058	fibroblast growth	345	121.5	6.7	474	1	C39667	brain-derived neur
273	133	7.4	825	2	A55178	neurotrophin recep	346	121.5	6.7	476	1	B39667	brain-derived neur
274	133	7.4	839	1	I73632	neurotrophin-3 rec	347	121.5	6.7	520	1	S44099	brain-derived neur
275	132.5	7.3	273	2	B28928	pregnancy-specific	348	121.5	6.7	818	1	S44098	brain-derived neur
276	132.5	7.3	275	2	A28928	pregnancy-specific	349	121.5	6.7	821	1	A39667	brain-derived neur
277	132.5	7.3	584	2	I50419	s-glycerin precu	350	121.5	6.7	1450	2	A44027	165K myofibrillar
278	132.5	7.3	856	2	I58411	protein-tyrosine k	351	121	6.7	292	2	T44044	glycoprotein [impo
279	132	7.3	1048	2	T30815	platelet-derived g	352	121	6.7	733	2	I49293	fibroblast growth
280	131.5	7.3	480	2	B56182	fibroblast growth	353	121	6.7	994	2	I49276	c-mer tyrosine kin
281	131.5	7.3	707	2	A38429	keratinocyte growt	354	121	6.7	1142	2	C36845	myosin-binding pro
282	131	7.3	499	2	S33766	platelet-derived g	355	120.5	6.7	212	2	C33258	pregnancy-specific
283	131	7.3	811	2	PN0889	connectin 1 - chic	356	120.5	6.7	353	2	S51242	heparin-binding fi
284	131	7.3	1106	1	PFHUGB	platelet-derived g	357	120.5	6.7	1742	2	S24600	projectin - fruit
285	130.5	7.2	310	2	JL0119	PC gamma (IgG) rec	358	120	6.6	729	2	A56795	fibroblast growth
286	130.5	7.2	323	2	S06946	PC gamma (IgG) rec	359	119.5	6.6	684	2	S60266	novel antigen rece
287	130	7.2	802	1	TVHUP4	fibroblast growth	360	119.5	6.6	6805	2	S20901	titin - rabbit (fr
288	129.5	7.2	419	2	A36109	pregnancy-specific	361	119	6.6	707	2	JC7763	neural leucine-r
289	129.5	7.2	707	2	A54846	fibroblast growth	362	119	6.6	820	2	S17295	fibroblast growth
290	129.5	7.2	1040	2	A57638	receptor tyrosine	363	119	6.6	860	2	JC5702	Erbb kinase activa
291	129.5	7.2	1103	2	T22889	hypothetical prote	364	119	6.6	868	2	JC5701	Erbb kinase activa
292	129	7.1	392	1	RWHUPD	poliovirus recepto	365	119	6.6	1274	2	S55050	cardiac myosin-bin
293	129	7.1	417	1	RWHUPA	poliovirus recepto	366	118	6.5	1451	2	S42167	190K protein - hum
294	129	7.1	1058	1	PFMSRB	platelet-derived g	367	117.5	6.5	182	2	I83053	pregnancy-specific
295	128.5	7.1	682	1	A53969	heparin-binding gr	368	117.5	6.5	335	2	A35514	pregnancy-specific
296	128	7.1	806	1	TVHUF3	fibroblast growth	369	117.5	6.5	569	2	A36187	interleukin-1 rece
297	127.5	7.1	241	2	S32359	glial growth facto	370	117.5	6.5	978	1	A49814	protein-tyrosine k
298	127	7.0	992	2	A39931	protein-tyrosine k	371	117	6.5	621	2	B57431	myosin-binding C-p
299	126.5	7.0	592	2	S25705	Ig mu chain - shee	372	117	6.5	825	1	A40026	neurotrophin-3 rec
300	126.5	7.0	790	2	A39627	protein-tyrosine k	373	117	6.5	894	1	A41527	protein-tyrosine k
301	126	7.0	477	1	I73631	brain-derived neur	374	116.5	6.5	243	2	A37982	calcium vector pro
302	126	7.0	822	1	A56853	brain-derived neur	375	116.5	6.5	282	2	T17219	hypothetical prote
303	126	7.0	940	2	A40985	projectin - fruit	376	116.5	6.5	317	2	JL0118	PC gamma (IgG) rec
304	126	7.0	1000	2	S18827	Flt3 protein - mou	377	116.5	6.5	599	2	T16774	hypothetical prote
305	125.5	6.9	251	2	T15495	hypothetical prote	378	116	6.4	253	2	T15475	hypothetical prote
306	125.5	6.9	278	2	JC1507	biliary glycoprote	379	116	6.4	268	2	T23555	hypothetical prote
307	125.5	6.9	335	2	B33251	nonspecific cross-	380	116	6.4	330	2	I46691	CD86 precursor - r
308	125.5	6.9	341	2	JC1511	biliary glycoprote	381	116	6.4	416	2	A54017	colon carcinoma-as
309	125.5	6.9	518	2	JC4024	poliovirus recepto	382	116	6.4	993	2	A36873	protein-tyrosine k
310	125.5	6.9	526	2	S70587	butyrophilin precu	383	115.5	6.4	526	2	A37821	butyrophilin - bov
311	125.5	6.9	975	1	TVMSKT	protein-tyrosine k	384	115.5	6.4	942	2	S23251	protein-tyrosine k
312	125	6.9	278	2	JC1506	biliary glycoprote	385	115	6.4	166	2	A33402	pregnancy-specific
313	125	6.9	341	2	JC1512	biliary glycoprote	386	115	6.4	813	1	A49123	fibroblast growth
314	125	6.9	977	2	I45877	protein-tyrosine k	387	115	6.4	1462	1	B36182	protein-tyrosine-p
315	124.5	6.9	750	2	S41051	fibroblast growth	388	114.5	6.3	326	2	JC4124	pregnancy-specific
316	124.5	6.9	829	2	JC4583	fibroblast growth	389	114	6.3	302	2	C36464	fibroblast growth
317	124.5	6.9	960	1	JN0677	protein-tyrosine k	390	114	6.3	432	1	RWMQT4	T-cell surface gly
318	124	6.9	278	2	A30337	carcinoembryonic a	391	114	6.3	713	2	I50128	fibroblast growth
319	124	6.9	426	2	C55181	pregnancy-specific	392	114	6.3	947	1	B44294	unc-5 protein, lon
320	124	6.9	426	2	S09016	pregnancy-specific	393	114	6.3	1132	2	A35089	myosin-binding pro
321	124	6.9	426	2	B35334	pregnancy-specific	394	113.5	6.3	344	2	A41357	PC gamma (IgG) rec

395	113.5	6.3	374	1	A39878	Fc gamma (IgG) rec	468	100	5.5	395	2	T05906	probable polygalac
396	113.5	6.3	547	1	S28904	intercellular adhe	469	100	5.5	531	2	S06016	intercellular adhe
397	113.5	6.3	1465	2	S43529	165K protein, skel	470	100	5.5	537	2	I49769	intercellular adhe
398	113	6.3	530	2	A53437	poliovirus recepto	471	100	5.5	641	2	D71170	hypothetical prote
399	112.5	6.2	304	1	RWCJH7	cell surface glyco	472	99	5.5	537	2	A45815	intercellular adhe
400	112.5	6.2	503	2	JC5287	SHP substrate-1 pr	473	99	5.5	869	2	T44440	chitinase (EC 3.2.
401	112.5	6.2	666	2	H89581	protein dim-1 limp	474	99	5.5	1160	2	F88369	protein unc-52 (im
402	112.5	6.2	954	2	I51703	c-kit-related kina	475	98.5	5.5	629	2	A46500	ly-9.2 antigen - m
403	112.5	6.2	2109	2	E89066	protein H05009.1 [	476	98	5.4	238	2	A49633	ly-9.2 antigen - m
404	112.5	6.2	2109	2	T33247	hypothetical prote	477	98	5.4	524	2	JQ0683	type-specific anti
405	112	6.2	573	2	S12838	Ig mu chain precu	478	98	5.4	544	2	JC5018	intercellular adhe
406	112	6.2	1327	2	T09402	immunoglobulin-lik	479	98	5.4	773	1	ORREG	secretory componen
407	111.5	6.2	335	2	C54312	pregnancy-specific	480	98	5.4	1000	2	I46521	titin - rabbit (fr
408	111.5	6.2	392	2	B44194	poliovirus recepto	481	97.5	5.4	197	2	PQ0327	heparin-binding fi
409	111.5	6.2	417	2	A44194	poliovirus recepto	482	97.5	5.4	270	2	S65739	basigin precursor
410	111.5	6.2	567	2	S29498	lymphocyte antigen	483	97	5.4	172	2	B26414	95K nonspecific cr
411	111	6.1	210	2	JC4122	pregnancy-specific	484	97	5.4	465	2	B97235	deacetylase/diipe
412	111	6.1	292	2	T44230	hypothetical prote	485	97	5.4	874	2	T29548	hypothetical prote
413	111	6.1	388	2	S17428	interleukin-1 rece	486	96.5	5.3	309	2	I49503	B-lymphocyte activ
414	111	6.1	748	2	S41050	fibroblast growth	487	96.5	5.3	364	2	T46926	hypothetical prote
415	110.5	6.1	509	2	JC5288	SHP substrate-1 pr	488	96.5	5.3	437	2	A64488	hypothetical prote
416	110.5	6.1	513	2	SJ5289	SHP substrate-1 pr	489	96.5	5.3	475	2	I76668	pregnancy-specific
417	110	6.1	285	2	S36903	Fc gamma (IgG) rec	490	96.5	5.3	580	2	A46538	Ig heavy chain, se
418	110	6.1	508	2	A33378	fasciclin III prec	491	96.5	5.3	709	2	A35364	carcinoembryonic a
419	110	6.1	919	2	T32541	unc-5 protein - Ca	492	96	5.3	455	1	MHMS	Ig mu chain C regi
420	110	6.1	1579	2	B91290	probable invasin [	493	96	5.3	455	2	A24976	Ig mu chain C regi
421	110	6.1	1700	2	G86131	probable invasin 2	494	96	5.3	476	1	MHMSM	Ig mu chain C regi
422	109.5	6.1	164	2	T19795	hypothetical prote	495	96	5.3	562	2	G02426	interleukin-1 rece
423	109.5	6.1	196	2	T19794	hypothetical prote	496	96	5.3	790	1	TVHUTT	nerve growth facto
424	109.5	6.1	206	2	A40305	biliary glycoprote	497	95.5	5.3	309	2	S15674	cell surface glyco
425	109.5	6.1	470	2	S22080	Ig heavy chain pre	498	95.5	5.3	330	2	A29915	teratocarcinoma gl
426	109.5	6.1	532	1	A29849	intercellular adhe	499	95.5	5.3	345	2	A46052	vascular cell adhe
427	108	6.0	207	2	A56190	titin - rat (fragm	500	95.5	5.3	375	2	I60125	PDGF receptor beta
428	108	6.0	267	2	I72882	Fc gamma receptor	501	95	5.3	267	2	A35902	gene MAC25 protein
429	108	6.0	467	1	HLMSR3	poliovirus recepto	502	95	5.3	277	2	I52825	prostaglandin-stimu
430	108	6.0	474	1	OMHUIB	alpha-1-8-glycopro	503	95	5.3	282	2	S50031	fibroblast growth
431	107.5	6.0	352	2	I77374	pregnancy-specific	504	95	5.3	329	2	A44065	nerve growth facto
432	107.5	6.0	404	2	A46480	Fc gamma (IgG) rec	505	95	5.3	799	1	TVRTTB	large repetitive p
433	107.5	6.0	537	2	A46611	myosin-binding pro	506	95	5.3	3283	2	AC1018	pregnancy-specific
434	106.5	5.9	336	2	S42632	Fit-1S protein pre	507	94.5	5.2	182	2	A34647	kinase-related pro
435	106.5	5.9	367	1	MHCH	Ig mu chain C regi	508	94.5	5.2	355	2	T72174	D9R protein - vari
436	106	5.9	407	2	T08732	hypothetical prote	509	94.5	5.2	1184	2	T09484	cartilage intermed
437	105.5	5.8	326	2	T37450	interleukin-1 beta	510	94.5	5.2	1280	2	AB1981	hypothetical prote
438	105.5	5.8	487	2	T28804	hypothetical prote	511	94.5	5.2	1452	1	S17670	protein-tyrosine-p
439	105	5.8	131	2	T20334	hypothetical prote	512	94.5	5.2	2347	1	TVHURS	kinase-related pro
440	105	5.8	269	2	A46506	leukocyte activati	513	94	5.2	328	2	I47159	Ig gamma 2a chain
441	104.5	5.8	290	2	F42527	B16R protein - vac	514	94	5.2	757	2	I45956	polymeric immunogl
442	104	5.8	1471	2	T19506	hypothetical prote	515	93.5	5.2	194	2	T29925	hypothetical prote
443	103.5	5.7	240	2	JC4121	pregnancy-specific	516	93.5	5.2	265	2	A55811	carcinoembryonic a
444	103.5	5.7	326	1	MMV215	BL5R protein precu	517	93.5	5.2	354	2	A46877	B20R protein - var
445	103.5	5.7	487	2	S65133	butyrophilin - mou	518	93.5	5.2	354	2	T28616	hypothetical prote
446	103.5	5.7	531	2	S20900	titin - mouse (fra	519	93.5	5.2	1366	2	B84924	hypothetical prote
447	103.5	5.7	538	2	T08093	PRR2 delta - human	520	93	5.1	144	2	B40098	colorectal cancer
448	103	5.7	618	2	T08685	hypothetical prote	521	93	5.1	267	2	I56110	Fc-gamma RIIB-alp
449	103	5.7	943	2	B45082	neutrophilic recep	522	93	5.1	299	2	I46690	CD80 precursor - r
450	102.5	5.7	257	2	S00682	IgG Fc receptor al	523	93	5.1	352	2	T33433	hypothetical prote
451	102.5	5.7	336	2	I48471	Fc gamma (IgG) rec	524	93	5.1	393	2	S16844	titin - rabbit (fr
452	102.5	5.7	1021	2	I39207	leukocyte surface	525	92.5	5.1	213	2	JE0247	Ig lambda chain NI
453	102	5.6	351	1	SAV2VW	surface antigen pr	526	92.5	5.1	274	2	T32736	hypothetical prote
454	102	5.6	478	2	I53960	PRR2 alpha - human	527	92.5	5.1	298	2	H64247	translation elonga
455	102	5.6	1398	2	T25568	hypothetical prote	528	92.5	5.1	590	2	I56526	interleukin 1 rece
456	101.5	5.6	275	2	JC7604	CD86 spliced varia	529	92.5	5.1	1220	2	T32916	hypothetical prote
457	101.5	5.6	329	1	A48754	B7-2 antigen - hum	530	92	5.1	328	2	I47160	Ig gamma 2b chain
458	101.5	5.6	625	1	T16777	hypothetical prote	531	92	5.1	460	2	JC2194	vasoactive intesti
459	101.5	5.6	937	2	SA5082	neutrophilic recep	532	92	5.1	545	2	JU0341	intercellular adhe
460	101	5.6	351	1	SAV2WR	surface antigen pr	533	91.5	5.1	455	2	H96797	hypothetical prote
461	101	5.6	353	1	SAV2VC	surface antigen pr	534	91	5.0	132	2	S14077	Ig kappa chain - A
462	101	5.6	421	1	T46286	hypothetical prote	535	91	5.0	370	2	A96741	hypothetical prote
463	101	5.6	458	1	RWHUT4	T-cell surface gly	536	91	5.0	416	2	S33473	interleukin-1 rece
464	101	5.6	751	2	I48748	semaphorin E - mou	537	91	5.0	427	2	G02034	killer cell inhibi
465	100.5	5.6	274	2	A47639	OX-2 membrane gly	538	90.5	5.0	391	2	T09058	thymophilin homol
466	100	5.5	235	2	S20000	Ig light chain pre	539	90.5	5.0	1269	2	F90538	hypothetical prote
467	100	5.5	304	2	B88746	protein C18P3.3 [i	540	90	5.0	283	1	FCMSG1	Fc gamma (IgG) rec

541	90	5.0	296	2	146021	FC-gamma receptor	614	85	4.7	1526	2	T19473	hypothetical prote
542	90	5.0	432	1	RWCZ74	T-cell surface gly	615	85	4.7	2274	2	T30258	adenomatous polypo
543	90	5.0	444	2	G01924	KIR (Cl-2) NK rece	616	85	4.7	2339	2	S41121	acetyl-CoA carboxy
544	90	5.0	576	2	A32604	interleukin-1 rece	617	85	4.7	4351	2	T00252	MEGF1 protein - ra
545	90	5.0	721	2	C82939	virulence associat	618	84.5	4.7	240	2	S01299	OX-45 membrane gly
546	90	5.0	858	1	VCLJG2	env polypeptide pr	619	84.5	4.7	243	2	A53244	leukocyte antigen
547	90	5.0	1357	2	T29265	hypothetical prote	620	84.5	4.7	330	2	A40071	PC gamma (IgG) rec
548	90	5.0	2282	2	T42717	DNA-binding protei	621	84.5	4.7	330	2	I49660	PC gamma-1/gamma-2
549	89.5	5.0	131	2	F45893	T-cell receptor al	622	84.5	4.7	385	2	T01332	hypothetical prote
550	89.5	5.0	245	2	JL0154	IgG receptor alpha	623	84.5	4.7	466	2	AF0172	asparagine-tRNA li
551	89.5	5.0	254	1	AJ0107	PC gamma (IgG) rec	624	84.5	4.7	727	2	S54512	hypothetical prote
552	89.5	5.0	362	2	A56745	microfibril-associ	625	84.5	4.7	897	2	E65127	probable bifunctio
553	89.5	5.0	1134	1	JN0711	protein-tyrosine k	626	84.5	4.7	1133	2	T01757	hypothetical prote
554	89.5	5.0	1691	1	D54689	protein-tyrosine-p	627	84.5	4.7	1227	2	T48028	hypothetical prote
555	89	4.9	257	2	P80401	basigin type II -	628	84	4.7	136	1	KWS21	Ig kappa chain pre
556	89	4.9	271	2	S43512	GP42/basigin prote	629	84	4.7	162	2	I51668	tumor suppressor -
557	89	4.9	273	2	JX0107	basigin precursor	630	84	4.7	225	2	G89336	conserved hypoteth
558	89	4.9	275	2	PS0402	basigin type III -	631	84	4.7	240	2	JL0143	antigen BCM1 precu
559	89	4.9	429	1	EHRT	Ig epsilon chain C	632	84	4.7	246	2	A29523	T-cell surface gly
560	89	4.9	598	2	A57249	beta-galactosidase	633	84	4.7	337	2	AG0963	hypothetical prote
561	89	4.9	769	1	QRRTGS	secretory componen	634	84	4.7	466	2	JCS897	killer cell inhibi
562	89	4.9	1452	1	S17669	protein-tyrosine-p	635	84	4.7	495	2	JC2195	vasoactive intesti
563	88.5	4.9	309	2	I49522	gene B7-2 protein	636	84	4.7	737	2	I39547	S-protein secretio
564	88	4.9	331	2	T15587	hypothetical prote	637	84	4.7	997	2	D75012	hypothetical prote
565	88	4.9	757	1	S48841	secretory componen	638	84	4.7	1442	2	S72441	protein-tyrosine-p
566	88	4.9	832	2	AD1096	internalin protein	639	84	4.7	1477	2	B43855	high-molecular-wei
567	88	4.9	4436	2	E71086	hypothetical prote	640	84	4.7	1536	2	A43855	high-molecular-wei
568	87.5	4.8	151	2	T31607	hypothetical prote	641	83.5	4.6	110	2	B30583	T-cell receptor de
569	87.5	4.8	280	2	I55577	PC gamma (IgG) rec	642	83.5	4.6	134	2	S21917	Ig kappa chain V r
570	87.5	4.8	321	2	I54766	B-lymphocyte activ	643	83.5	4.6	245	2	T07071	beta-fructofuranos
571	87.5	4.8	368	2	S17980	psal protein - Asp	644	83.5	4.6	315	1	HNV24X	hemagglutinin prec
572	87.5	4.8	402	2	T29703	hypothetical prote	645	83.5	4.6	328	2	S30444	ST2 protein - huma
573	87.5	4.8	660	2	H71376	probable tpr.prote	646	83.5	4.6	374	2	S69339	Ig heavy chain V r
574	87	4.8	359	2	A97119	undecaprenyl-pp-Mu	647	83.5	4.6	405	1	B42606	cytochrome P450 CV
575	87	4.8	383	2	T21946	hypothetical prote	648	83.5	4.6	490	2	B96952	sucrase-6-phosphat
576	87	4.8	477	2	B64115	asparagine-tRNA li	649	83.5	4.6	513	2	F86320	hypothetical prote
577	87	4.8	814	2	I40048	S-layer protein pr	650	83.5	4.6	583	2	S57721	capB protein - Clo
578	87	4.8	974	1	A49714	protein-tyrosine k	651	83.5	4.6	1054	2	T18304	acid trehalase hom
579	87	4.8	2458	2	T17420	probable polyketid	652	83.5	4.6	1557	2	T25421	hypothetical prote
580	86.5	4.8	235	2	S25058	Ig kappa chain - m	653	83	4.6	220	2	A49444	Ig gamma-1 heavy c
581	86.5	4.8	278	1	TDRTOX	OX-2 membrane gly	654	83	4.6	313	2	JQ1862	31r protein - vari
582	86.5	4.8	440	2	D71175	hypothetical prote	655	83	4.6	315	1	HNV2V	hemagglutinin prec
583	86.5	4.8	1533	2	T00344	hypothetical prote	656	83	4.6	410	2	C69197	ATP-dependent 26S
584	86	4.8	387	2	T04320	polysaccharuronase	657	83	4.6	555	2	JQ1526	interleukin-1 rece
585	86	4.8	387	2	T07391	polysaccharuronase	658	83	4.6	563	2	C95874	conserved hypoteth
586	86	4.8	444	2	G01925	KIR (Cl-11) NK rec	659	83	4.6	633	2	AE2312	transketolase limp
587	86	4.8	501	1	A60005	glycoprotein A pre	660	83	4.6	680	2	JCS895	killer cell inhibi
588	86	4.8	501	1	VBENBA	glycoprotein A pre	661	83	4.6	767	2	S41479	DNA-binding protei
589	86	4.8	501	1	VBENBH	glycoprotein gp57-	662	83	4.6	1014	2	T24412	hypothetical prote
590	86	4.8	505	1	A968BH	hypothetical prote	663	83	4.6	1033	2	AI2359	hypothetical prote
591	86	4.8	580	2	A968B3	hypothetical prote	664	83	4.6	2338	1	A42545	genome polypeptid
592	86	4.8	587	2	S36231	beta-fructofuranos	665	83	4.6	4836	2	T14346	herc2 protein - mo
593	86	4.8	856	1	A44963	env polypeptide pr	666	82.5	4.6	125	2	A53627	fibroblast growth
594	86	4.8	1394	2	S60762	IgA-specific serin	667	82.5	4.6	160	2	I47163	cytolytic trigger
595	86	4.8	1711	2	AB1283	peptidoglycan link	668	82.5	4.6	193	2	JCS593	Ig kappa chain (WM
596	85.5	4.7	475	2	A54879	pregnancy-specific	669	82.5	4.6	237	2	JCS5322	p53 specific singl
597	85.5	4.7	510	2	PC4054	cardiac C-protein	670	82.5	4.6	247	1	RWMST2	T-cell surface gly
598	85.5	4.7	593	1	DTCHPH	purH bifunctional	671	82.5	4.6	315	2	T37438	hemagglutinin - va
599	85.5	4.7	764	1	QRHUGS	secretory componen	672	82.5	4.6	429	2	T36088	probable secreted
600	85.5	4.7	1145	1	GNLJEV	HIV-1 retropepsin	673	82.5	4.6	433	2	S31436	Ig upsilon chain -
601	85.5	4.7	1146	1	GNLJ22	HIV-1 retropepsin	674	82.5	4.6	610	2	T25262	hypothetical prote
602	85.5	4.7	1146	1	GNLJEW	HIV-1 retropepsin	675	82.5	4.6	871	2	H81430	translation initia
603	85.5	4.7	1732	2	T30836	lysine-specific cy	676	82.5	4.6	1553	2	T18502	hypothetical prote
604	85	4.7	505	2	B48831	hypothetical prote	677	82	4.5	120	2	D29775	Ig kappa chain pre
605	85	4.7	635	2	JCS896	killer cell inhibi	678	82	4.5	225	2	I51335	Ig lambda chain -
606	85	4.7	753	2	B36268	platelet glycoprot	679	82	4.5	230	2	S49449	Ig lambda chain -
607	85	4.7	778	2	A60798	platelet glycoprot	680	82	4.5	270	2	A34636	PC-gamma receptor
608	85	4.7	788	2	I77349	platelet glycoprot	681	82	4.5	288	2	A45803	B-cell-restricted
609	85	4.7	788	2	A26547	platelet glycoprot	682	82	4.5	313	2	H36854	hemagglutinin - va
610	85	4.7	817	2	A48721	titin, muscle - ch	683	82	4.5	318	2	V72171	K9r protein - vari
611	85	4.7	832	2	E71492	hypothetical prote	684	82	4.5	489	1	VGBETA	glycoprotein A - t
612	85	4.7	939	2	I41197	ease protein (enter	685	82	4.5	523	1	A60408	glycoprotein gp57-
613	85	4.7	1436	2	JCS290	protein-tyrosine-p	686	82	4.5	630	2	T38637	hypothetical prote

687	82	4.5	663	1	ORECIC	colicin I receptor	760	79.5	4.4	290	2	C97533	pyruvate dehydroge
688	82	4.5	820	2	Tl4879	hypothetical prote	761	79.5	4.4	306	2	AE2752	pyruvate dehydroge
689	82	4.5	841	2	JC5894	killer cell inhibi	762	79.5	4.4	468	1	A1242	interleukin-6 rece
690	82	4.5	842	2	T04555	hypothetical prote	763	79.5	4.4	474	2	I50830	Ig mu chain - Lepi
691	82	4.5	1125	1	S57846	protein-tyrosine k	764	79.5	4.4	522	2	B42804	immunodominant typ
692	82	4.5	1222	2	T22490	hypothetical prote	765	79.5	4.4	558	2	A44964	apical membrane an
693	82	4.5	1577	2	T30858	glucosyltransferas	766	79.5	4.4	653	2	A49722	endoglin precursor
694	81.5	4.5	107	2	PL0268	Ig kappa chain V r	767	79.5	4.4	766	1	CDHU26	diptidyl-peptida
695	81.5	4.5	240	2	A41797	Ig light chain - s	768	79.5	4.4	1022	1	S00503	Na+/K+-exchanging
696	81.5	4.5	247	2	A34954	T-cell surface gly	769	79.5	4.4	1034	1	A53663	enteropeptidase (E
697	81.5	4.5	259	2	JC7109	sr2v protein - hum	770	79.5	4.4	1036	2	B6368	hypothetical prote
698	81.5	4.5	656	2	T23338	hypothetical prote	771	79.5	4.4	1156	2	T23308	hypothetical prote
699	81.5	4.5	1183	2	A89135	protein F25G6.2 [1	772	79.5	4.4	1185	2	A42404	collagen adhesin -
700	81.5	4.5	1203	2	S27455	pullulanase - Ther	773	79.5	4.4	1409	2	T42522	protein-tyrosine-p
701	81.5	4.5	1336	2	T17479	hypothetical prote	774	79.5	4.4	1422	2	T30111	hypothetical prote
702	81.5	4.5	1983	2	G86643	hypothetical prote	775	79	4.4	91	2	S17638	Ig kappa chain V r
703	81	4.5	234	2	S14237	Ig kappa chain pre	776	79	4.4	101	2	H37262	Ig heavy chain V r
704	81	4.5	247	2	A55717	myelin/oligodendro	777	79	4.4	231	2	S27553	Ig lambda chain -
705	81	4.5	314	1	HN2VW	hemagglutinin prec	778	79	4.4	348	2	C81284	cystathionine beta
706	81	4.5	314	1	JQ1793	hemagglutinin prec	779	79	4.4	370	2	G97001	endogalactosidase fami
707	81	4.5	451	2	S71754	cellular hepatitis	780	79	4.4	387	2	T04322	polylacturonase
708	81	4.5	545	2	A38447	oligopeptide ABC t	781	79	4.4	403	2	T20727	hypothetical prote
709	81	4.5	568	2	A45804	Ig mu chain C regi	782	79	4.4	432	2	S30193	T-cell surface gly
710	81	4.5	571	2	H69584	acetolactate synth	783	79	4.4	450	2	B97292	probable ATP-depen
711	81	4.5	578	2	B96883	hypothetical prote	784	79	4.4	474	1	G2MS11	Ig gamma-2b chain
712	81	4.5	585	2	A46507	Ig alpha chain - c	785	79	4.4	659	2	G91009	colicin I receptor
713	81	4.5	588	2	C83836	subtilisin-type pr	786	79	4.4	753	2	G02173	semaphorin III fam
714	81	4.5	637	2	B83052	DnaK protein PA476	787	79	4.4	807	2	A71663	DNA gyrase chain B
715	81	4.5	665	2	E86775	ribonuclease (impo	788	79	4.4	875	2	H90371	proteinase [import
716	80.5	4.5	248	1	QOB84L	probable glycoprot	789	79	4.4	1175	2	D85089	hypothetical prote
717	80.5	4.5	269	2	B97501	hypothetical prote	790	79	4.4	1204	2	C75015	probable Pyrolysin
718	80.5	4.5	273	2	G89856	conserved hypotet	791	79	4.4	1350	2	AF2005	RNA polymerase bet
719	80.5	4.5	277	2	T14762	Ig gamma 4 chain c	792	79	4.4	1439	2	T27110	hypothetical prote
720	80.5	4.5	298	2	T30086	hypothetical prote	793	78.5	4.3	111	2	D37266	Ig kappa chain V r
721	80.5	4.5	327	2	B97076	UDP-glucose 4-epim	794	78.5	4.3	115	2	B46518	Ig l1 chain V regi
722	80.5	4.5	358	2	A99214	sUA5 related conse	795	78.5	4.3	140	2	PH1498	Ig heavy chain V r
723	80.5	4.5	459	2	A46254	CD4 precursor - ra	796	78.5	4.3	228	2	S29575	Ig light chain - r
724	80.5	4.5	466	2	AF0816	asparagine-tRNA li	797	78.5	4.3	290	1	X1RBM	lysylamine N-acetyl
725	80.5	4.5	517	2	B87644	4-coumarate-CoA li	798	78.5	4.3	323	2	JC2578	DNA repair protein
726	80.5	4.5	554	2	A91250	probable portal pr	799	78.5	4.3	373	2	JH0155	pectin lyase (BC 4
727	80.5	4.5	596	2	D84972	ABC transporter At	800	78.5	4.3	392	2	T03229	enoyl-[acyl]-carrie
728	80.5	4.5	613	2	T41565	hypothetical prote	801	78.5	4.3	434	2	S72430	transcription elon
729	80.5	4.5	881	2	S67026	probable membrane	802	78.5	4.3	434	2	D88305	protein R03D7.4 [i
730	80.5	4.5	1025	2	G81722	polymorphic membra	803	78.5	4.3	553	1	SMEBH1	flagellar hook-ass
731	80.5	4.5	1128	1	T08312	plasmid replicatio	804	78.5	4.3	553	2	AH0640	flagellar hook-ass
732	80.5	4.5	1349	2	S51471	killer toxin insen	805	78.5	4.3	556	2	A44441	B-cell antigen CD1
733	80.5	4.5	1375	2	TJ0345	dextranucrase (EC	806	78.5	4.3	561	2	T45607	hypothetical prote
734	80.5	4.5	1433	2	T30261	chitinase (EC 3.2.	807	78.5	4.3	590	2	A56535	gadd34 protein - l
735	80.5	4.5	1457	1	A48066	protein-tyrosine-p	808	78.5	4.3	592	2	S54489	phosphoribosylamin
736	80.5	4.5	1538	2	E70874	probable ppeB prot	809	78.5	4.3	605	1	A48665	methylmalonyl-CoA
737	80.5	4.5	4588	2	T28667	dynein beta heavy	810	78.5	4.3	668	2	JQ0773	penicillin-binding
738	80	4.4	104	2	JH0345	T-cell receptor al	811	78.5	4.3	693	2	S46417	heat shock protein
739	80	4.4	150	2	A40862	fibroblast growth	812	78.5	4.3	759	2	B90520	ABC transporter at
740	80	4.4	233	2	I51383	Ig lambda chain -	813	78.5	4.3	783	2	AG3402	polyphosphate kina
741	80	4.4	239	2	G02630	pCalpharb - human	814	78.5	4.3	829	2	B87305	polyphosphate kina
742	80	4.4	287	2	JH0332	IgA (Fc) receptor,	815	78.5	4.3	934	2	B29838	parasporal crystal
743	80	4.4	313	2	T28598	hypothetical prote	816	78.5	4.3	1019	2	T40813	probable cell divi
744	80	4.4	425	2	JE0086	SH3-domain binding	817	78.5	4.3	1070	2	T34385	hypothetical prote
745	80	4.4	433	1	S48515	adenylosuccinate s	818	78.5	4.3	1217	2	T00270	hypothetical prote
746	80	4.4	454	1	MHY9	Ig mu chain C regi	819	78.5	4.3	1252	2	T31119	mshQ protein - Vib
747	80	4.4	466	2	H96991	secreted protein c	820	78.5	4.3	1385	2	A88554	protein C38C10.5b
748	80	4.4	522	2	S42253	probable Nbl prote	821	78.5	4.3	1391	2	B88554	protein C38C10.5b
749	80	4.4	642	2	S44542	probable membrane	822	78.5	4.3	1440	2	JC6312	protein-tyrosine-p
750	80	4.4	680	2	PN0510	integrin beta-3 ch	823	78.5	4.3	1687	2	T43144	vitellogenin II pr
751	80	4.4	937	2	T04194	hypothetical prote	824	78.5	4.3	1687	2	B85547	probable RTX famil
752	80	4.4	995	2	A56599	hypothetical prote	825	78.5	4.3	5188	2	F90696	hypothetical prote
753	80	4.4	1200	2	T48194	embryo kinase 5 -	826	78	4.3	5291	2	S62676	herregulin isoform
754	80	4.4	3343	2	T42207	hypothetical prote	827	78	4.3	125	2	PT0178	Ig kappa chain pre
755	79.5	4.4	155	2	A41675	telokin - rabbit	828	78	4.3	131	2	PT0178	Ig light chain V r
756	79.5	4.4	204	2	A69197	hypothetical prote	829	78	4.3	132	2	A55410	T-cell receptor al
757	79.5	4.4	220	2	I55937	Lyt-2.1 lymphocyte	830	78	4.3	137	2	C45893	hypothetical prote
758	79.5	4.4	250	2	A34342	IgG Fc receptor al	831	78	4.3	233	2	S29577	Ig light chain - r
759	79.5	4.4	261	2	S29360	Fc gamma (IgG) rec	832	78	4.3	255	2	JC7593	SH2 domain-contain



833	78	4.3	301	1	G64491	thioedoxin-disulf	906	76.5	4.2	267	1	RWMS8	T-cell receptor al
834	78	4.3	320	2	I47158	Ig gamma 1 chain c	907	76.5	4.2	239	1	AHRB	Ig alpha chain C r
835	78	4.3	378	1	HLHUA3	MHC class I histoc	908	76.5	4.2	236	2	B75129	thiamin biosynthes
836	78	4.3	413	2	AG3267	amino-acid N-acety	909	76.5	4.2	332	2	D83745	3-oxoacyl-lacyl-ca
837	78	4.3	460	2	S67174	hypothetical prote	910	76.5	4.2	403	2	S53477	IMP dehydrogenase
838	78	4.3	475	2	T44566	conserved hypotet	911	76.5	4.2	428	2	AH3536	dihydrofolamide S
839	78	4.3	481	2	E82217	asparaginyl-trNA s	912	76.5	4.2	431	2	A86601	hypothetical prote
840	78	4.3	542	2	A84554	hypothetical prote	913	76.5	4.2	431	2	G72022	probable sodium-tr
841	78	4.3	702	2	T21148	hypothetical prote	914	76.5	4.2	457	2	A27449	T-cell surface gly
842	78	4.3	874	2	G84513	Mutator-like trans	915	76.5	4.2	463	2	T14884	hypothetical prote
843	78	4.3	980	2	H90681	probable flagellin	916	76.5	4.2	483	2	A69745	hypothetical prote
844	78	4.3	980	2	D85532	probable outer mem	917	76.5	4.2	515	2	H86202	hypothetical prote
845	78	4.3	1016	2	H71460	probable structure	918	76.5	4.2	516	2	H70035	levanase homolog y
846	78	4.3	1029	2	F96602	hypothetical prote	919	76.5	4.2	528	2	PC4025	intercellular adhe
847	78	4.3	1138	1	S24066	protein-tyrosine k	920	76.5	4.2	547	2	S75904	hypothetical prote
848	78	4.3	1217	2	F97177	alpha-glucosidase	921	76.5	4.2	563	2	T20631	hypothetical prote
849	78	4.3	2185	1	GNNYSV	genome polyprotein	922	76.5	4.2	572	1	HNNZB3	hemagglutinin-neur
850	78	4.3	2256	2	AD1018	large repetitive p	923	76.5	4.2	573	2	F89719	protein F09812.1 (
851	78	4.3	4302	2	A38971	polycystic kidney	924	76.5	4.2	573	2	T20632	hypothetical prote
852	77.5	4.3	119	2	PH1519	Ig heavy chain V r	925	76.5	4.2	622	2	A36915	fructanase - Bacte
853	77.5	4.3	140	2	A36194	Ig heavy chain V r	926	76.5	4.2	653	2	B90908	probable host spec
854	77.5	4.3	284	2	S75817	hypothetical prote	927	76.5	4.2	656	2	B71290	conserved hypotet
855	77.5	4.3	307	2	C71002	hypothetical prote	928	76.5	4.2	740	2	AD0485	probable exported
856	77.5	4.3	309	2	T15747	hypothetical prote	929	76.5	4.2	749	2	E86774	hypothetical prote
857	77.5	4.3	315	1	HN5ZVT	hemagglutinin prec	930	76.5	4.2	775	2	G90996	probable host spec
858	77.5	4.3	428	2	T48167	hypothetical prote	931	76.5	4.2	782	2	A85693	hypothetical prote
859	77.5	4.3	446	2	S40295	Ig gamma-2a chain	932	76.5	4.2	896	2	T22061	hypothetical prote
860	77.5	4.3	466	2	C85619	asparagine tRNA sy	933	76.5	4.2	913	2	E75554	valyl-tRNA synthet
861	77.5	4.3	466	2	E90755	asparagine tRNA sy	934	76.5	4.2	1039	2	T30856	protein F2 - Strept
862	77.5	4.3	469	1	T7HUE2	transcription fact	935	76.5	4.2	1124	1	I58388	protein-tyrosine k
863	77.5	4.3	532	2	C42804	immunodominant typ	936	76.5	4.2	1131	2	T14517	hypothetical prote
864	77.5	4.3	534	2	S60205	phosphonoacetaldeh	937	76.5	4.2	1151	2	S48431	probable membrane
865	77.5	4.3	584	2	F70522	probable polyketid	938	76.5	4.2	1248	2	C89874	autolysin (impor
866	77.5	4.3	593	2	A11235	internalin prote	939	76.5	4.2	1363	2	C84346	hypothetical prote
867	77.5	4.3	655	2	T34219	hypothetical prote	940	76.5	4.2	1377	2	I54632	tsh protein - Esch
868	77.5	4.3	668	2	S49639	probable membrane	941	76.5	4.2	1648	2	S61654	probable membrane
869	77.5	4.3	676	2	T30480	envelope protein h	942	76.5	4.2	2477	2	S14428	fibronectin precu
870	77.5	4.3	852	1	VCLJGG	env polyprotein pr	943	76	4.2	91	2	PH1071	Ig light chain V r
871	77.5	4.3	888	2	A54280	cell differentiat	944	76	4.2	107	2	PD0011	Ig kappa chain V r
872	77.5	4.3	1192	2	T08609	hypothetical prote	945	76	4.2	108	2	G30560	Ig kappa chain V r
873	77.5	4.3	1474	2	F69009	probable membrane	946	76	4.2	108	2	S38720	Ig kappa chain V r
874	77.5	4.3	1515	2	A40303	4-alpha-glucanotra	947	76	4.2	118	2	I33932	Ig kappa chain pre
875	77.5	4.3	1819	2	D97033	uncharacterized pr	948	76	4.2	120	2	C29775	Ig kappa chain pre
876	77.5	4.3	1825	2	C88400	protein H19W22.1 (	949	76	4.2	161	2	S04931	T-cell receptor de
877	77.5	4.3	1825	2	T32828	hypothetical prote	950	76	4.2	251	2	S64927	probable membrane
878	77.5	4.3	3329	2	T42205	breast cancer susc	951	76	4.2	254	2	B75052	coenzyme pqq synth
879	77.5	4.3	3329	2	T30904	breast cancer tumo	952	76	4.2	310	2	F90011	conserved hypotet
880	77.5	4.3	3591	1	S21010	filamentous hemag	953	76	4.2	327	2	T07104	2'-hydroxydihydro
881	77	4.3	107	2	PC4405	Ig kappa chain V r	954	76	4.2	327	2	S06611	Ig gamma-2 chain C
882	77	4.3	128	2	S40343	Ig kappa chain V-J	955	76	4.2	365	2	D87526	hypothetical prote
883	77	4.3	234	2	S01320	Ig kappa chain pre	956	76	4.2	426	2	H84846	probable polygalac
884	77	4.3	302	2	S50579	hypothetical prote	957	76	4.2	430	2	T28143	tapasin 1 homolog,
885	77	4.3	328	2	I47161	Ig gamma 3 chain c	958	76	4.2	431	2	F71476	probable sodium-tr
886	77	4.3	338	2	S09276	Ig alpha chain C r	959	76	4.2	450	1	MHDG	Ig mu chain C regi
887	77	4.3	384	2	E84871	probable polygalac	960	76	4.2	473	2	E83676	pyruvate dehydroge
888	77	4.3	439	2	AE1251	probable peptidogl	961	76	4.2	501	2	E96509	protein F27F5.17 (
889	77	4.3	614	2	A88466	protein B0244.2 (i	962	76	4.2	506	1	ACRYG1	nicotinic acetylch
890	77	4.3	817	2	F86742	ribonuclease (limp	963	76	4.2	511	2	E84685	probable seed stor
891	77	4.3	859	2	AC2089	adenylate cyclase	964	76	4.2	516	2	A44494	cAMP-responsive el
892	77	4.3	879	2	C90879	hypothetical prote	965	76	4.2	577	2	T48530	clathrin binding p
893	77	4.3	879	2	G85739	hypothetical prote	966	76	4.2	656	2	AC0429	2',3'-cyclic-nucle
894	77	4.3	928	2	A87749	protein F55C7.7c (	967	76	4.2	859	1	VCLJCT	env polyprotein pr
895	77	4.3	976	2	C96958	ACT domain contain	968	76	4.2	1020	2	A46405	C.protein alpha an
896	77	4.3	1071	1	PXBIVA	H+-exporting ATPas	969	76	4.2	1151	2	S03722	DNA-directed DNA p
897	77	4.3	1176	2	A33856	surface-layer 125X	970	76	4.2	1196	2	H86389	hypothetical prote
898	77	4.3	2488	2	T42739	guanine nucleotide	971	76	4.2	1278	2	A47462	probable DNA-direc
899	77	4.3	3562	2	A47171	chondroitin sulfat	972	76	4.2	1366	2	S57664	IgA-specific metal
900	76.5	4.2	135	2	PH1492	Ig heavy chain V r	973	76	4.2	2380	2	T29551	hypothetical prote
901	76.5	4.2	136	2	A49137	Ig kappa chain pre	974	75.5	4.2	104	2	JC6076	anti-D-dimer monoc
902	76.5	4.2	178	2	S29594	Ig kappa chain (MW	975	75.5	4.2	114	2	S44119	Ig kappa chain V-J
903	76.5	4.2	232	2	S17399	Ig lambda chain pr	976	75.5	4.2	123	2	S35479	Ig kappa chain pre
904	76.5	4.2	236	2	A24637	T-cell surface gly	977	75.5	4.2	131	2	S09259	Ig kappa chain pre
905	76.5	4.2	252	2	AF2719	arginine-tRNA-prot	978	75.5	4.2	131	2	D29380	Ig kappa chain pre

979	75.5	4.2	132	2	PH0106	anti-digoxin trans	1052	75	4.2	1311	2	T33757	hypothetical prote
980	75.5	4.2	133	2	S40324	Ig kappa chain V r	1053	75	4.2	1313	2	G82887	hypothetical prote
981	75.5	4.2	140	1	HVMSG7	Ig heavy chain pre	1054	75	4.2	1476	2	AC2220	hypothetical prote
982	75.5	4.2	140	2	PH1489	Ig heavy chain V r	1055	75	4.2	1661	2	H71439	hypothetical prote
983	75.5	4.2	189	2	T39849	anaphase promoting	1056	75	4.2	1672	2	T46237	hypothetical prote
984	75.5	4.2	231	2	PC4155	Ig gamma-2b chain	1057	75	4.2	2291	2	S11238	polymerase - Berne
985	75.5	4.2	234	2	A39956	Ig lambda chain pr	1058	75	4.2	2413	2	S34670	splicing factor PR
986	75.5	4.2	248	2	F96655	hypothetical prote	1059	75	4.2	2500	2	G71609	hypothetical prote
987	75.5	4.2	249	2	C69081	acetyl-CoA synthet	1060	74.5	4.1	116	1	HVMS1B	Ig heavy chain pre
988	75.5	4.2	262	2	T42986	v-cyclin - ateline	1061	74.5	4.1	119	2	PH1517	Ig heavy chain V r
989	75.5	4.2	316	2	F86157	hypothetical prote	1062	74.5	4.1	119	2	PH1516	Ig heavy chain V r
990	75.5	4.2	341	2	S72445	DNA-binding protei	1063	74.5	4.1	140	2	PH1488	Ig heavy chain V r
991	75.5	4.2	362	2	S16303	polygalacturonase	1064	74.5	4.1	192	2	T02893	hypothetical prote
992	75.5	4.2	398	2	T46475	hypothetical prote	1065	74.5	4.1	232	2	S25756	Ig lambda chain -
993	75.5	4.2	402	2	F70850	DNA-directed DNA p	1066	74.5	4.1	243	2	AC3071	transcription regu
994	75.5	4.2	504	2	S00390	Ig gamma chain (cl	1067	74.5	4.1	277	2	S29922	Sal1eL protein pre
995	75.5	4.2	524	2	D87440	2-isopropylmalate	1068	74.5	4.1	370	1	HVRKC5	Ig mu chain C regi
996	75.5	4.2	569	2	A46462	T cell activation	1069	74.5	4.1	397	2	S70987	dnaN protein - Myc
997	75.5	4.2	580	2	S49308	beta-fructofuranos	1070	74.5	4.1	438	2	B97712	hypothetical prote
998	75.5	4.2	582	2	S53814	DEAD box protein -	1071	74.5	4.1	466	1	SYECNT	asparagine-tRNA li
999	75.5	4.2	641	2	JC7142	dextranase (EC 3.2	1072	74.5	4.1	468	1	P2ML51	L2 protein - human
1000	75.5	4.2	691	1	S46735	NADPH-ferrihemopro	1073	74.5	4.1	501	2	S74341	hypothetical prote
1001	75.5	4.2	710	1	A46273	mitochondrial inte	1074	74.5	4.1	549	2	S04845	Ig heavy chain pre
1002	75.5	4.2	713	1	ALBSG7	cyclomaltodextrin	1075	74.5	4.1	591	1	CB8Y2	L-lactate dehydrog
1003	75.5	4.2	739	2	A55314	glycine-tRNA ligas	1076	74.5	4.1	644	2	S05552	hypothetical prote
1004	75.5	4.2	746	2	E64701	conserved hypoteth	1077	74.5	4.1	663	2	AG0782	colicin I receptor
1005	75.5	4.2	771	2	B70564	hypothetical prote	1078	74.5	4.1	693	2	JN0843	heat shock protein
1006	75.5	4.2	815	2	AB2444	hypothetical prote	1079	74.5	4.1	729	2	T46270	hypothetical prote
1007	75.5	4.2	857	1	S05943	gelation factor -	1080	74.5	4.1	807	2	T39479	histone transcript
1008	75.5	4.2	918	2	D71407	hypothetical prote	1081	74.5	4.1	862	2	E88594	protein Y48A6B.11
1009	75.5	4.2	1068	2	S73091	hypothetical prote	1082	74.5	4.1	899	2	A83019	conserved hypoteth
1010	75.5	4.2	1787	2	A99273	hypothetical prote	1083	74.5	4.1	947	2	T26314	hypothetical prote
1011	75.5	4.2	1818	2	AE3011	conserved hypoteth	1084	74.5	4.1	1043	2	D84900	hypothetical prote
1012	75.5	4.2	1871	2	D96698	probable DNA polym	1085	74.5	4.1	1183	2	S63046	probable membrane
1013	75.5	4.2	1894	2	T02155	DNA-directed DNA p	1086	74.5	4.1	1403	2	T11583	hypothetical prote
1014	75.5	4.2	2265	1	FNBO	fibronectin - bovi	1087	74.5	4.1	1622	2	T45240	hypothetical prote
1015	75.5	4.2	2505	2	S82884	hypothetical prote	1088	74.5	4.1	1825	2	S13507	microtubule-associ
1016	75.5	4.2	6669	2	F55024	nebulin, skeletal	1089	74.5	4.1	1830	2	A37981	microtubule-associ
1017	75	4.2	106	2	A49138	IgA kappa rheumato	1090	74.5	4.1	2338	2	I73957	kinase-related pro
1018	75	4.2	115	2	B26524	T-cell receptor be	1091	74.5	4.1	2366	2	S10317	toxin B - Clostrid
1019	75	4.2	117	2	S40362	Ig kappa chain - h	1092	74.5	4.1	2761	2	T21064	hypothetical prote
1020	75	4.2	128	2	A47159	Ig lambda chain v	1093	74.5	4.1	4572	2	S57908	hypothetical 57K
1021	75	4.2	130	2	C29380	Ig kappa chain pre	1094	74.5	4.1	4639	1	A54794	dyein heavy chain
1022	75	4.2	131	2	D34904	Ig kappa chain pre	1095	74	4.1	107	2	S12954	Ig kappa chain V r
1023	75	4.2	148	2	PH0115	Ig heavy chain pre	1096	74	4.1	108	2	T26681	hypothetical prote
1024	75	4.2	157	2	D31327	IgG receptor alpha	1097	74	4.1	131	2	S52449	Ig kappa chain V r
1025	75	4.2	215	2	A57843	sodium channel bet	1098	74	4.1	196	2	S72716	4-coumarate-CoA li
1026	75	4.2	246	2	B69230	hypothetical prote	1099	74	4.1	221	1	Q0B848	BARF1 protein - hu
1027	75	4.2	268	2	A56446	Ig heavy chain V r	1100	74	4.1	231	2	S25751	Ig lambda chain -
1028	75	4.2	283	2	AH1767	protoporphyrinogen	1101	74	4.1	248	2	B45831	MHC class I histoc
1029	75	4.2	285	2	B82842	spermidine synthas	1102	74	4.1	277	2	D42521	A38L protein - vac
1030	75	4.2	297	2	AC2380	hypothetical prote	1103	74	4.1	365	2	I37476	MHC class I histoc
1031	75	4.2	307	1	RWMSBC	T-cell receptor be	1104	74	4.1	365	2	I56039	HLA-A30.3 precurs
1032	75	4.2	321	2	S10006	hypothetical prote	1105	74	4.1	365	2	I38519	MHC class I histoc
1033	75	4.2	359	2	AF3184	beta-lactamase [im	1106	74	4.1	416	1	A41267	transcription fact
1034	75	4.2	364	2	S03535	class I histocompa	1107	74	4.1	429	2	AC1522	flagellar hook-ass
1035	75	4.2	392	2	T34095	zinc finger protei	1108	74	4.1	438	1	HVRKCS	Ig mu chain C regi
1036	75	4.2	393	2	T03216	enoyl-[acyl-carrie	1109	74	4.1	449	1	B64706	hemolysin - Helic
1037	75	4.2	394	2	G69230	endo-1,4-beta-gluc	1110	74	4.1	454	2	T26296	hypothetical prote
1038	75	4.2	416	2	B64140	hypothetical prote	1111	74	4.1	461	1	HVRKC0	Ig mu chain C regi
1039	75	4.2	435	2	T42613	probable envelope	1112	74	4.1	468	1	TVMSE2	transcription fact
1040	75	4.2	439	2	G97159	contains cell adhe	1113	74	4.1	474	2	T47299	hypothetical prote
1041	75	4.2	444	2	B90053	hypothetical prote	1114	74	4.1	514	2	G89903	conserved hypoteth
1042	75	4.2	476	2	S64291	hypothetical prote	1115	74	4.1	523	2	F85489	2-isopropylmalate
1043	75	4.2	479	1	VGBER2	glycoprotein F - h	1116	74	4.1	523	2	F90638	2-isopropylmalate
1044	75	4.2	535	2	S76564	hypothetical prote	1117	74	4.1	523	2	B64729	hypothetical prote
1045	75	4.2	574	2	T29005	hypothetical prote	1118	74	4.1	562	2	AH2084	hypothetical prote
1046	75	4.2	577	2	I50731	Ig heavy chain - n	1119	74	4.1	573	2	T02743	lactase (EC 1.10.3
1047	75	4.2	701	2	C97910	ATP-dependent prot	1120	74	4.1	579	2	D87063	probable acyl-CoA
1048	75	4.2	743	2	T34853	probable fusidic a	1121	74	4.1	587	2	S63033	hypothetical prote
1049	75	4.2	775	1	JQ1639	outer layer protei	1122	74	4.1	701	2	C97302	hypothetical prote
1050	75	4.2	780	2	T31548	hypothetical prote	1123	74	4.1	755	2	T48553	subtilisin-like pr
1051	75	4.2	1242	1	DJBEC1	DNA-directed DNA p	1124	74	4.1	876	2	T51507	WD40-repeat protei

1125	74	4.1	879	2	H64888	membrane protein y	1198	73	4.0	469	2	D95989	conserved hypochet
1126	74	4.1	908	2	T25035	hypothetical prote	1199	73	4.0	478	2	S47040	gene Tt52 protein
1127	74	4.1	966	2	E87473	ATP-dependent rec	1200	73	4.0	481	2	C97238	ATP-dependent RNA
1128	74	4.1	1085	2	JC2227	probable helicase	1201	73	4.0	523	2	A12696	serine proteinase
1129	74	4.1	1128	2	H90538	hypothetical prote	1202	73	4.0	523	2	A97479	probable serine pr
1130	74	4.1	1132	1	OSBPL	host specificity p	1203	73	4.0	565	2	H69342	GTP-binding protei
1131	74	4.1	1136	1	S57845	protein-tyrosine k	1204	73	4.0	586	2	T45945	laccase-like prote
1132	74	4.1	1137	2	R90734	probable host spec	1205	73	4.0	657	2	AD1525	probable cell surf
1133	74	4.1	1482	2	S13495	pregnancy zone pro	1206	73	4.0	671	2	T23015	hypothetical prote
1134	74	4.1	1488	2	C70984	probable ppsa proc	1207	73	4.0	673	2	H86761	hypothetical prote
1135	74	4.1	1524	2	A96950	DNA segregation AT	1208	73	4.0	673	2	T41768	glycine-cRNA ligas
1136	74	4.1	1963	2	B98002	IgA-specific metal	1209	73	4.0	688	2	S39491	AcMNPV orf23 - Bom
1137	74	4.1	2185	1	GNVSH	genome polyprotein	1210	73	4.0	701	2	H95039	prochlorophyllid
1138	74	4.1	2812	2	T43271	phosphotidylinosit	1211	73	4.0	722	2	D70200	hypothetical prote
1139	73.5	4.1	64	2	S20961	keratinocyte growt	1212	73	4.0	745	2	B33856	polynucleotide
1140	73.5	4.1	96	2	PH1070	Ig light chain v r	1213	73	4.0	754	2	E86592	hypothetical 80K p
1141	73.5	4.1	97	2	T26341	Ig light chain v r	1214	73	4.0	754	2	D72032	general secretion
1142	73.5	4.1	119	2	PH1510	Ig heavy chain v r	1215	73	4.0	771	2	AF2056	general secretion
1143	73.5	4.1	119	2	PH1518	Ig heavy chain v r	1216	73	4.0	772	2	A46108	cation transportin
1144	73.5	4.1	133	2	PC1155	Ig heavy chain pre	1217	73	4.0	858	2	T12142	outer capsid prote
1145	73.5	4.1	135	2	PH1493	Ig heavy chain v r	1218	73	4.0	870	2	T47454	lipoxigenase (EC 1
1146	73.5	4.1	140	2	PH1486	Ig heavy chain v r	1219	73	4.0	896	2	JQ2391	lipoxigenase ALOX
1147	73.5	4.1	140	2	PH1483	Ig heavy chain v r	1220	73	4.0	897	2	S67283	lipoxigenase (EC 1
1148	73.5	4.1	229	2	A20969	Ig kappa chain pre	1221	73	4.0	935	2	S66306	hypothetical prote
1149	73.5	4.1	309	2	T09564	glutaminyl-peptide	1222	73	4.0	980	2	T39630	valine-tRNA ligase
1150	73.5	4.1	339	2	T28138	Ig V-region-like B	1223	73	4.0	1095	2	T24061	hypothetical prote
1151	73.5	4.1	340	2	T28137	Ig V-region-like B	1224	73	4.0	1336	2	T18288	hypothetical prote
1152	73.5	4.1	366	2	AF0497	DNA-directed DNA p	1225	73	4.0	1473	2	A35186	ABC transport prot
1153	73.5	4.1	380	2	S12839	Ig heavy chain pre	1226	73	4.0	1518	2	T28880	salivary agglutini
1154	73.5	4.1	388	2	E95007	sugar isomerase do	1227	73	4.0	1815	2	B95942	hypothetical prote
1155	73.5	4.1	400	2	T22853	probable cathepsin	1228	73	4.0	2207	2	S09553	conserved hypochet
1156	73.5	4.1	418	2	G87469	ThiJ/PfpI family p	1229	73	4.0	2210	1	RRXPTV	genome polyprotein
1157	73.5	4.1	422	2	A96912	glutamate-1-semial	1230	73	4.0	2807	2	A57278	fibillin-2 precur
1158	73.5	4.1	431	2	S37775	filamin, muscle -	1231	73	4.0	3011	1	S40770	genome polyprotein
1159	73.5	4.1	505	2	AC3486	cell surface prote	1232	73	4.0	3263	2	E82410	hypothetical prote
1160	73.5	4.1	579	2	B84956	cell division prot	1233	73	4.0	4688	2	F82885	hypothetical prote
1161	73.5	4.1	632	2	C98264	5'-nucleotidase pr	1234	73	4.0	4936	2	AH2515	hypothetical prote
1162	73.5	4.1	636	2	AF3020	5'-nucleotidase li	1235	72.5	4.0	124	2	S40364	Ig kappa chain - h
1163	73.5	4.1	677	2	T40145	probable beta-adap	1236	72.5	4.0	126	2	S40312	Ig kappa chain - h
1164	73.5	4.1	725	2	C87485	ComEC/Rec2 family	1237	72.5	4.0	128	2	S20636	Ig kappa chain v r
1165	73.5	4.1	815	2	E70021	3-hydroxyacyl-CoA	1238	72.5	4.0	137	2	E34903	Ig heavy chain pre
1166	73.5	4.1	941	2	S29043	cellulase (EC 3.2.	1239	72.5	4.0	141	2	I47178	Ig heavy chain var
1167	73.5	4.1	986	2	B81675	polymorphic membra	1240	72.5	4.0	198	2	T19797	hypothetical prote
1168	73.5	4.1	1005	2	T18537	Ig heavy chain - c	1241	72.5	4.0	199	2	G75153	hypothetical prote
1169	73.5	4.1	1052	2	H83909	cell wall-associat	1242	72.5	4.0	215	2	I64004	hypothetical prote
1170	73.5	4.1	1119	2	A86340	protein F2D10.24 l	1243	72.5	4.0	219	2	S38865	Ig kappa chain - m
1171	73.5	4.1	1121	2	I38127	phosphoprotein pho	1244	72.5	4.0	233	1	JU0284	Fc gamma (IgG) rec
1172	73.5	4.1	1280	2	T00365	hypothetical prote	1245	72.5	4.0	247	2	PQ0655	outer capsid spike
1173	73.5	4.1	1285	2	B72420	hypothetical prote	1246	72.5	4.0	247	2	PQ0656	outer capsid spike
1174	73.5	4.1	1292	2	T09229	galactose binding	1247	72.5	4.0	247	2	PQ0657	outer capsid spike
1175	73.5	4.1	1310	1	QGFPE	epidermal growth f	1248	72.5	4.0	264	2	T27579	T-cell receptor al
1176	73.5	4.1	1487	2	S15904	alpha-1 proteinase	1249	72.5	4.0	267	2	PL0064	T-cell receptor be
1177	73.5	4.1	1571	2	T00062	hypothetical prote	1250	72.5	4.0	286	2	S32480	hypothetical prote
1178	73.5	4.1	3328	2	T30835	breast cancer tumo	1251	72.5	4.0	288	2	S29690	Ig heavy chain VDJ
1179	73	4.0	126	2	S24704	Ig heavy chain V6	1252	72.5	4.0	289	2	G00031	B7 protein - red-c
1180	73	4.0	127	2	PH1224	Ig kappa chain pre	1253	72.5	4.0	312	2	D82690	adenine-specific m
1181	73	4.0	128	2	PN0445	Ig kappa chain pre	1254	72.5	4.0	322	2	T50167	hypothetical prote
1182	73	4.0	131	2	E25733	T-cell receptor al	1255	72.5	4.0	350	2	T21106	hypothetical prote
1183	73	4.0	132	2	E27632	T-cell receptor al	1256	72.5	4.0	377	2	T05453	trehalose-6-phosph
1184	73	4.0	133	1	K4HUJ1	Ig kappa chain pre	1257	72.5	4.0	401	2	E87531	probable ABC trans
1185	73	4.0	145	2	S21651	T-cell receptor be	1258	72.5	4.0	408	2	D95417	hypothetical prote
1186	73	4.0	225	2	B82473	hypothetical prote	1259	72.5	4.0	423	2	F64436	hypothetical prote
1187	73	4.0	233	2	S25747	Ig lambda chain -	1260	72.5	4.0	428	2	B84964	adenosylmethionine
1188	73	4.0	332	2	G83458	sulfate-binding pr	1261	72.5	4.0	451	2	T48340	hypothetical prote
1189	73	4.0	349	2	T08782	hypothetical prote	1262	72.5	4.0	453	2	C31933	Ig mu chain C regi
1190	73	4.0	389	2	B42708	serine-type D-Ala-	1263	72.5	4.0	475	2	S01321	Ig gamma-2b chain
1191	73	4.0	393	1	HVRXC1	Ig mu chain C regi	1264	72.5	4.0	482	2	T49079	serine-type carbox
1192	73	4.0	438	1	HVRXC2	Ig mu chain C regi	1265	72.5	4.0	498	2	G97279	protein containing
1193	73	4.0	445	1	S67695	26S proteasome reg	1266	72.5	4.0	503	2	B72289	oligopeptide ABC t
1194	73	4.0	451	1	S75239	hypothetical prote	1267	72.5	4.0	527	2	T22000	hypothetical prote
1195	73	4.0	454	2	AE1970	hypothetical prote	1268	72.5	4.0	533	2	A42249	aspartic proteinas
1196	73	4.0	469	1	P2WL35	L2 protein - human	1269	72.5	4.0	560	2	B81451	flagellar M-ring p
1197	73	4.0	469	2	S36525	L2 protein - human	1270	72.5	4.0	668	2	T05803	hypothetical prote

1271	72.5	4.0	676	2	F69276	conserved hypother	1344	72	4.0	992	2	T46337	hypothetical prote
1272	72.5	4.0	736	2	D96830	probable heat-shoc	1345	72	4.0	1076	1	A35622	nuclear pore prote
1273	72.5	4.0	759	1	B60008	RNA-directed RNA p	1346	72	4.0	1083	2	S48460	probable membrane
1274	72.5	4.0	836	2	A69550	hypothetical prote	1347	72	4.0	1106	2	A97647	cation efflux syst
1275	72.5	4.0	887	1	IJCHCL	E-cadherin precurs	1348	72	4.0	1106	2	AG2870	Acr family transpo
1276	72.5	4.0	894	2	S61015	hypothetical prote	1349	72	4.0	1132	2	H90834	host specificity p
1277	72.5	4.0	941	2	F97353	uncharacterized co	1350	72	4.0	1149	2	T27567	hypothetical prote
1278	72.5	4.0	954	2	S57108	hypothetical prote	1351	72	4.0	1155	2	H71456	probable pyrolysin
1279	72.5	4.0	970	2	T78842	receptor protein-t	1352	72	4.0	1199	2	S77082	pyruvate (flavodox
1280	72.5	4.0	1039	2	T15885	hypothetical prote	1353	72	4.0	1245	1	VHWVB2	structural polypro
1281	72.5	4.0	1166	2	T29009	hypothetical prote	1354	72	4.0	1391	2	S50608	hypothetical prote
1282	72.5	4.0	1186	2	T42729	histocompatibility	1355	72	4.0	1408	2	H69068	cell surface glyco
1283	72.5	4.0	1212	2	T42387	histocompatibility	1356	72	4.0	2094	2	S33124	tpir protein - huma
1284	72.5	4.0	1228	2	G90581	hypothetical prote	1357	72	4.0	2567	2	A49551	filamin, Muller ce
1285	72.5	4.0	1229	2	T25697	hypothetical prote	1358	72	4.0	2902	2	C71953	toxin-like outer m
1286	72.5	4.0	1276	2	B86546	polymorphic outer	1359	72	4.0	3890	2	C89921	hypothetical prote
1287	72.5	4.0	1276	2	C81591	polymorphic membra	1360	72	4.0	8563	2	T30226	polyketide synthas
1288	72.5	4.0	1305	2	S22624	aggregation protei	1361	71.5	4.0	91	2	S17628	Ig kappa chain v r
1289	72.5	4.0	1383	2	T13052	guanine nucleotide	1362	71.5	4.0	119	2	PH1503	Ig heavy chain v r
1290	72.5	4.0	1431	2	A45866	dextranucrase (EC	1363	71.5	4.0	121	2	S44113	Ig heavy chain v r
1291	72.5	4.0	1500	1	JQ11348	carbamoyl-phosphat	1364	71.5	4.0	129	2	S40347	Ig kappa chain - h
1292	72.5	4.0	1665	2	T29008	hypothetical prote	1365	71.5	4.0	225	2	JL0029	Ig kappa chain pre
1293	72.5	4.0	1966	2	T08991	hypothetical prote	1366	71.5	4.0	246	1	A32999	myelin P0 protein
1294	72.5	4.0	2004	2	F95133	immunoglobulin A1	1367	71.5	4.0	275	2	H35216	FP31 protein - fow
1295	72.5	4.0	2052	2	C97038	phage-related prot	1368	71.5	4.0	275	2	C82752	hypothetical prote
1296	72.5	4.0	3924	2	S37431	ankyrin 2, neurona	1369	71.5	4.0	290	2	T40852	cystathionine beta
1297	72.5	4.0	4845	2	T31067	BIR repeat contain	1370	71.5	4.0	303	2	H71693	hypothetical prote
1298	72	4.0	115	1	KVMSK2	Ig kappa chain pre	1371	71.5	4.0	305	2	B84413	hypothetical prote
1299	72	4.0	115	2	A30995	Ig kappa chain pre	1372	71.5	4.0	321	2	F71163	probable oligopept
1300	72	4.0	111	2	B34904	Ig kappa chain pre	1373	71.5	4.0	325	2	H90269	hypothetical prote
1301	72	4.0	111	2	B30577	Ig kappa chain pre	1374	71.5	4.0	326	1	G2HU	Ig gamma-2 chain C
1302	72	4.0	133	2	T45927	membrane-bound imm	1375	71.5	4.0	340	2	S20879	homeotic protein H
1303	72	4.0	148	2	PH0121	Ig heavy chain pre	1376	71.5	4.0	360	2	H95980	probable uroporphyr
1304	72	4.0	148	2	PH0119	Ig heavy chain pre	1377	71.5	4.0	361	2	S78542	drpDglucose 4,6-de
1305	72	4.0	208	1	WMNV15	18.5K protein - Au	1378	71.5	4.0	384	2	A12962	cellulose synthesi
1306	72	4.0	223	2	I46696	CTLA-4 precursor -	1379	71.5	4.0	389	2	E98320	hypothetical prote
1307	72	4.0	239	2	F81795	probable periplasm	1380	71.5	4.0	476	2	A46118	myosin-binding pro
1308	72	4.0	338	2	A53066	CCAR enhancer-bin	1381	71.5	4.0	477	2	JC4386	adenylyl cyclase-a
1309	72	4.0	340	2	T02639	G5 protein homolog	1382	71.5	4.0	493	2	S39299	hexon protein - hu
1310	72	4.0	349	2	F70357	lipoprotein - Aqu	1383	71.5	4.0	507	1	A43387	polymerase-associa
1311	72	4.0	351	2	JQ2166	spindle body prote	1384	71.5	4.0	507	2	AC3036	glycerol-3-phospha
1312	72	4.0	372	1	UHUUCN	ciliary neurotroph	1385	71.5	4.0	507	2	H98249	glpD gene homolog
1313	72	4.0	375	2	A64398	hypothetical prote	1386	71.5	4.0	520	2	A13295	adenylosuccinate s
1314	72	4.0	386	2	B84562	probable Tub famil	1387	71.5	4.0	523	1	S48997	IMP dehydrogenase
1315	72	4.0	411	1	VBEG2	glycoprotein G pre	1388	71.5	4.0	572	2	B46529	Ig Y heavy chain (
1316	72	4.0	411	2	A37755	xyylanase (EC 3.2.1	1389	71.5	4.0	592	2	JC4642	purH bifunctional
1317	72	4.0	424	2	H96963	dihydroorotase [im	1390	71.5	4.0	608	2	T32708	hypothetical prote
1318	72	4.0	425	2	AC2959	HlyD family secret	1391	71.5	4.0	611	2	T45493	glutamine-fructose
1319	72	4.0	428	2	T08826	sarcosine reductas	1392	71.5	4.0	647	2	F70057	penicillin-binding
1320	72	4.0	430	2	T32055	hypothetical prote	1393	71.5	4.0	659	2	S36551	El protein - human
1321	72	4.0	433	2	S76485	hypothetical prote	1394	71.5	4.0	668	2	T44118	penicillin-binding
1322	72	4.0	441	2	AF0048	modification methy	1395	71.5	4.0	668	2	JQ0774	penicillin-binding
1323	72	4.0	452	2	C98324	hypothetical prote	1396	71.5	4.0	751	2	A13392	phosphoribosylform
1324	72	4.0	454	2	A46532	Ig mu chain C regi	1397	71.5	4.0	775	1	I37422	glutamine-tRNA lig
1325	72	4.0	513	2	D96943	Probable polygalac	1398	71.5	4.0	775	2	A32494	transposable eleme
1326	72	4.0	515	2	AH2596	glycerol-3-phospha	1399	71.5	4.0	776	2	S59790	hypothetical prote
1327	72	4.0	531	2	A98287	glpD gene homolog	1400	71.5	4.0	860	2	AC0582	leucyl-tRNA syntht
1328	72	4.0	531	2	T50964	related to RCC1 pr	1401	71.5	4.0	893	2	F86476	protein F1504.39 [
1329	72	4.0	570	2	A27535	intrileukin 1 recep	1402	71.5	4.0	928	2	C97728	hypothetical prote
1330	72	4.0	574	2	T46261	hypothetical prote	1403	71.5	4.0	958	2	S32435	Na+/Ca2+-exchangin
1331	72	4.0	574	2	E64414	hypothetical prote	1404	71.5	4.0	1021	2	T15765	hypothetical prote
1332	72	4.0	576	2	C81657	DNA mismatch repai	1405	71.5	4.0	1025	2	T10259	RNA-directed DNA p
1333	72	4.0	627	2	S14683	Ig mu chain precur	1406	71.5	4.0	1031	2	D88912	protein T06A10.1 [
1334	72	4.0	665	2	F97032	beta-glucosidase f	1407	71.5	4.0	1031	2	T33655	hypothetical prote
1335	72	4.0	697	2	T27583	hypothetical prote	1408	71.5	4.0	1094	2	S22573	DNA-directed DNA p
1336	72	4.0	777	1	TVWPCP	large T antigen -	1409	71.5	4.0	1125	2	H87644	TonB-dependent rec
1337	72	4.0	782	2	S22560	large T antigen -	1410	71.5	4.0	1128	1	T08322	plasmid replicatio
1338	72	4.0	844	2	T37690	hypothetical prote	1411	71.5	4.0	1231	2	S30185	probable nuclear e
1339	72	4.0	844	2	T52396	formin-binding pro	1412	71.5	4.0	1250	2	T40062	probable nuclear e
1340	72	4.0	868	2	D86349	hypothetical prote	1413	71.5	4.0	1441	2	T13717	CRAG protein - fru
1341	72	4.0	878	1	RRXSIB	RNA-directed RNA p	1414	71.5	4.0	1446	2	S73013	polyketide synthas
1342	72	4.0	892	2	T06918	DNA topoisomerase	1415	71.5	4.0	1448	2	AI2007	Subtilase family p
1343	72	4.0	984	2	C84781	hypothetical prote	1416	71.5	4.0	1526	2	AC2239	WD-40 repeat prote

1417 71.5 4.0 1540 2 H87203 polyketide synthas  
1418 71.5 4.0 1592 2 S63208 hypothethical prote  
1419 71.5 4.0 1603 1 V3KW5 vitellogenin vit-5  
1420 71.5 4.0 1797 2 P69195 cell surface glyco  
1421 71.5 4.0 2013 2 A11439 probable peptidogl  
1422 71.5 4.0 2014 2 T36936 complement recepto  
1423 71.5 4.0 2670 1 UIHU thyroglobulin prec  
1424 71.5 4.0 3670 2 T36249 CDA peptide synthe  
1425 71.5 4.0 4342 2 H83343 probable non-ribos  
1426 71.5 4.0 4342 2 T32650 hypothethical prote  
1427 71.5 4.0 6359 2 T31679 bacitracin synthet  
1428 71.5 4.0 15281 2 S41309 cyclosporin synthe  
1429 71 3.9 115 1 K3HUCI Ig kappa chain pre  
1430 71 3.9 115 2 D27552 T-cell receptor be  
1431 71 3.9 115 2 T12517 hypothethical prote  
1432 71 3.9 128 2 S40373 Ig kappa chain - n  
1433 71 3.9 128 2 A56701 Ig kappa chain v r  
1434 71 3.9 131 2 B32513 Ig kappa chain pre  
1435 71 3.9 133 2 E82603 hypothethical prote  
1436 71 3.9 133 2 G32536 T-cell receptor al  
1437 71 3.9 148 2 PH0116 Ig heavy chain pre  
1438 71 3.9 197 2 T16627 hypothethical prote  
1439 71 3.9 223 2 T09536 cytotoxic T-lympho  
1440 71 3.9 224 2 F98215 transcription regu  
1441 71 3.9 240 2 S06084 Ig kappa chain pre  
1442 71 3.9 255 2 G83543 conserved hypotet  
1443 71 3.9 261 2 AC0164 probable transport  
1444 71 3.9 277 2 T37424 probable 31.5K pro  
1445 71 3.9 313 2 A34677 secretory pathway  
1446 71 3.9 313 2 B53290 oligopeptide trans  
1447 71 3.9 323 2 B72224 conserved hypotet  
1448 71 3.9 336 2 C83926 S-adenosylmethioni  
1449 71 3.9 344 2 A69325 hypothethical prote  
1450 71 3.9 356 2 T40041 hypothethical prote  
1451 71 3.9 357 2 E86823 peptidoglycan synt  
1452 71 3.9 368 2 G81289 UDPgalactopyranose  
1453 71 3.9 375 2 H86938 conserved hypotet  
1454 71 3.9 397 2 F66680 F5I14.10 [imported  
1455 71 3.9 400 2 T34363 hypothethical prote  
1456 71 3.9 404 2 AF2225 hypothethical prote  
1457 71 3.9 405 1 VGBEGF glycoprotein.G pre  
1458 71 3.9 429 2 AC1163 flagellar hook-ass  
1459 71 3.9 431 2 H81738 probable sodium-tr  
1460 71 3.9 440 2 JL0144 interleukin-6 rece  
1461 71 3.9 460 2 JL0145 interleukin-6 rece  
1462 71 3.9 462 2 S74579 carboxyl-terminal  
1463 71 3.9 472 2 AH3353 serine-type D-Ala-  
1464 71 3.9 476 2 T19786 hypothethical prote  
1465 71 3.9 478 2 H86100 hypothethical prote  
1466 71 3.9 482 2 AC0426 serine-type D-Ala-  
1467 71 3.9 501 2 T13316 hypothethical prote  
1468 71 3.9 503 2 T40650 hypothethical prote  
1469 71 3.9 507 2 JQ1929 phosphoprotein - r  
1470 71 3.9 516 2 F82070 2-isopropylmalate  
1471 71 3.9 522 2 B69116 conserved hypotet  
1472 71 3.9 642 2 G69371 acetyl-CoA synthet  
1473 71 3.9 646 2 T27899 hypothethical prote  
1474 71 3.9 659 2 A85854 hypothethical prote  
1475 71 3.9 660 2 AD0661 invasin-like prote  
1476 71 3.9 695 2 S66662 protein-glutamine  
1477 71 3.9 784 2 F97981 exoribonuclease R  
1478 71 3.9 786 2 F95977 protein tyrosine k  
1479 71 3.9 837 2 S43556 furin (EC 3.4.21.7  
1480 71 3.9 848 2 T28055 hypothethical prote  
1481 71 3.9 922 2 T40372 trp asp repeat pro  
1482 71 3.9 946 1 A29550 methylenetetrahydr  
1483 71 3.9 1015 2 S68141 nuclear protein HI  
1484 71 3.9 1032 2 T23164 hypothethical prote  
1485 71 3.9 1035 2 T23165 hypothethical prote  
1486 71 3.9 1036 2 T05687 beta-galactosidase  
1487 71 3.9 1057 2 T16676 hypothethical prote  
1488 71 3.9 1081 2 T15692 hypothethical prote

71 3.9 1144 2 A36968 pl-like adhesion pr  
71 3.9 1145 2 T05573 hypothethical prote  
71 3.9 1152 2 AC1347 probable peptidogl  
71 3.9 1288 2 B99789 hemagglutinin/hemo  
71 3.9 1270 2 E85649 hypothethical prote  
71 3.9 1341 2 S09579 tail fiber protein  
71 3.9 1500 1 SYRTCA carbamoyl-phosphat  
71 3.9 1555 2 S38758 amylase-alpha-1.6-gl  
71 3.9 2062 2 G96602 probable receptor  
71 3.9 2163 2 S50675 pre-mRNA splicing  
71 3.9 2183 2 T42764 coagulation factor

## ALIGNMENTS

## RESULT 1

I56551  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I56551  
R;Struyk, A.F.; Canoll, P.D.; Wolfgang, M.J.; Rosen, C.L.; D'Eustachio, P.; Salzer, J.L.  
J. Neurosci. 15, 2141-2156, 1995  
A;Title: Cloning of neurotrophin defines a new subfamily of differentially expressed neur  
A;Reference number: I56551; MUID:95198094; PMID:7891157  
A;Accession: I56551  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-344 <RES>  
C;Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin

Query Match 90.8%; Score 1639.5; DB 2; Length 344;

Best Local Similarity 92.9%; Pred. No. 2.5e-113;  
Matches 312; Conservative 9; Mismatches 12; Indels 3; Gaps 1;

QY 12 ISWAIFGTGLAALCLF--QGVPVRSQGDATFPKAMDVTVVRQGESATLRCTIDNRVTRVAV 68  
DB 9 LPWKLLVVSRLFLVPTGVPVRSQGDATFPKAMDVTVVRQGESATLRCTIDNRVTRVAV 68  
QY 69 LNRSTLYAGNDKWCIDPRVLLSNLTQYISIEIQNVVYDEGPTCSVQTDNHPKTSRV 128  
DB 69 LNRSTLYAGNDKWCIDPRVLLSNLTQYISIEIQNVVYDEGPTCSVQTDNHPKTSRV 128  
QY 129 HLIVQSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEI 188  
DB 129 HLIVQSPKIVEISSDISINEGNNISLTCTATGRPEPTVTRHISPKAVGFVSEDEYLEI 188  
QY 189 QGITRQSGDGYECSASNDVAAPVVRVVKTVVNPVYISBAKGTGVPVGOKGTQCEASAV 248  
DB 189 QGITRQSGEYECASNDVAAPVVRVVKTVVNPVYISBAKGTGVPVGOKGTQCEASAV 248  
QY 249 PSAEFQWYKDDKRLIEBKGGKVKVKNRPFLSKLIFFNVSEHDYGNVTCVASNKLGHNTASI 308  
DB 249 PSAEFQWYKDDKRLIEBKGGKVKVKNRPFLSKLIFFNVSEHDYGNVTCVASNKLGHNTASI 308  
QY 309 MLFPGGAVSEVNGTSRRAGCWLLPLLVLLHLLKF 344  
DB 309 MLFPGGAVSEVNGTSRRAGCWLLPLLVLLHLLKF 344

## RESULT 2

JC1238

C;Species: Rattus norvegicus (clone DU21) - rat

C;Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 09-Jul-2004

C;Accession: JC1238

R;Lippman, D.A.; Lee, N.M.; Loh, H.H.

Gene 117, 249-254, 1992

A;Title: Opioid-binding cell adhesion molecule (OBAM)-related clones from a rat brain c

A;Reference number: JC1238; MUID:92347701; PMID:1339369

A;Accession: JC1238







A31923  
amalgam protein precursor - fruit fly (Drosophila melanogaster)  
C/Species: Drosophila melanogaster  
C/Date: 18-Oct-1989 #sequence\_revision 18-Oct-1989 #text\_change 09-Jul-2004  
C/Accession: A31923  
R/Seeger, M.A.; Haffley, L.; Kaufman, T.C.  
Cell 55, 589-600, 1988  
A/Title: Characterization of amalgam: a member of the immunoglobulin superfamily from Dm  
A/Reference number: A31923; MUID:89028670; PMID:3141062  
A/Accession: A31923  
A/Molecule type: DNA  
A/Residues: 1-333 <SEE>  
A/Cross-references: UNIPROT:P15364; GB:M23561; NID:g156920; PIDN:AAA28367.1; PID:g156921  
C/Genetics:  
A/Genes: FlyBase:Ama  
A/Cross-references: FlyBase:FBgn0000071

Query Match 16.5%; Score 297.5; DB 2; Length 333;  
Best Local Similarity 29.7%; Pred. No. 1.5e-14;  
Matches 87; Conservative 43; Mismatches 136; Indels 27; Gaps 11;

Qy 44 NTVVROGESATLRCTIDN-RVTRVAVLNR-----STILYAGNDKMKCLDPR--VLLSN 93  
Db 33 DVVASVGDSVEFNCTVEEVGQLSVSWAKRPSSEDTNSVLSMRNILSLPKRYNVITVEG 92

Qy 94 TQTQ---YSTEIQNVVDGPGYTCVSQTDNHPK-TSRVHLIVQVSPKIVE-ISSDISIN 148  
Db 93 PKTGSALTTPRIQNIEMSDMGPEVCQVLVSATERKVTKLSIQIKTPPVIAPKSTLVT 152

Qy 149 EGNNISLTCTATGRPEPTVTRH---ISPKAVGFVSEDEYLEIQTITREOSGDYECAS 204  
Db 153 EGQMLETCHANGPKPTISWAREHNAVMP-AGHLLAEPTLRIRSVHRMDRGYYCIAQ 211

Qy 205 NDVAAPVVRVVKVTVNPPYIS-EAKGTGVPGVGKGTLOCEASAVPSAEQVYKDDKRLI 263  
Db 212 NGEQPKRLIRVEFRPQLAVQRPIAQMVSASHAELECSVQGPAPTVMHKGVP-L- 270

Qy 264 EGKKGKVENR-----PFLSKLFFNVSEHDYNYTCVASKNKLGHNTNASIMLF 311  
Db 271 QSSRHEVANTASSSGTTTSLRIDSVEEDFGDYCYCNATNKLGHADARLHLF 323

RESULT 9  
IJMSNG  
neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse  
N/Alternate names: NCAM-120  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
C/Accession: A29673; S00382; A44290  
R/Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Pontec  
EMBO J. 6, 907-914, 1987  
A/Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000  
A/Reference number: A29673; MUID:87246524; PMID:3595563  
A/Accession: A29673  
A/Molecule type: mRNA  
A/Residues: 1-725 <BAR>  
A/Cross-references: UNIPROT:P13594; EMBL:Y00051; NID:G53342; PIDN:CAA68263.1; PID:G53343  
R/Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.  
EMBO J. 7, 625-632, 1988  
A/Title: Differential splicing and alternative polyadenylation generates distinct NCAM t  
A/Reference number: S00382; MUID:98283628; PMID:3396534  
A/Accession: S00382  
A/Molecule type: DNA  
A/Residues: 642-656, 'D', 658-725 <BA2>  
A/Cross-references: EMBL:X07195  
R/Rougon, G.; Marshak, D.R.  
J. Biol. Chem. 261, 3396-3401, 1986  
A/Title: Structural and immunological characterization of the amino-terminal domain of m  
A/Reference number: A44290; MUID:86140120; PMID:3512556  
A/Accession: A44290  
A/Molecule type: protein  
A/Residues: 20-36 <ROU>  
C/Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol

C/Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IJMSR  
C/Genetics:  
A/Genes: NCAM  
A/Map position: 9  
A/Introns: 701/1  
C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu  
C/Keywords: alternative splicing; cell adhesion; duplication; heparin binding; membrane i  
F/1-19/Domain: signal sequence #status predicted <SIG>  
F/34-98/Domain: immunoglobulin homology <IMM1>  
F/132-191/Domain: immunoglobulin homology <IMM2>  
F/152-156/Region: heparin binding #status predicted  
F/161-165/Region: heparin binding #status predicted  
F/228-290/Domain: immunoglobulin homology <IMM3>  
F/263-272/Region: NCAM binding #status predicted  
F/323-388/Domain: immunoglobulin homology <IMM4>  
F/420-482/Domain: immunoglobulin homology <IMM5>  
F/519-596/Domain: fibronectin type III repeat homology <FN3A>  
F/625-685/Domain: fibronectin type III repeat homology <FN3B>  
F/41-96,139-189,235-286,330-386,427-480/Disulfide bonds: #status predicted  
F/222,316,348,424,450,479/Binding site: carbohydate (Asn) (covalent) #status predicted

Query Match 15.7%; Score 283.5; DB 1; Length 725;  
Best Local Similarity 25.8%; Pred. No. 4.4e-13;  
Matches 75; Conservative 45; Mismatches 130; Indels 41; Gaps 7;

Qy 44 NTVVROGESATLRCTIDN-RVTRVAVLNRSTILYAGNDKMKCLDPRV-----LLSNTQ 95  
Db 222 NATANLQSVTLVCDADG-----PPEPTM-----SWTKDGEPIENBEEDRSRSVS 268

Qy 96 TQVSIQIENVVVDGPGYTCVSQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNISL 155  
Db 269 DSSEVTIRNVKNDKDEAYVYICIAENKAGEQDASHLKVFAPKITYVENOTAMELEBQVTL 328

Qy 156 TCIATGRPEPTVTR-----HSPKAVGFVSEDEYLEIQTITREOSGDYE 200  
Db 329 TCEASGDPISITWRTSTRNISSEEDLDGHVMVRSHARVSS---LTKSLQIYRDAGEYM 385

Qy 201 CSASNDVAAPVVRVVKVTVNPPYISAEKGTGVPGVGKGTLOCEASAVPSAEQVYKDDK 260  
Db 386 CTASNTIGQD-SQSIDLEFQYAPKLOGPVAVVTWEGNQVNITCEVFAFPSATISWFRDQG 444

Qy 261 RLIEGK-KGVKVENRPFLSKLFFNVSEHDYNYTCVASKNKLGHNTNASIML 310  
Db 445 LLPSSNYSNIKIYNTPSASVLEVTDPSENDGYNCTAVNRIGQESLEFIL 495

RESULT 10  
IJMSNL  
neural cell adhesion molecule 1 precursor, long domain splice form - mouse  
N/Alternate names: NCAM-180  
N/Contains: neural cell adhesion molecule, short domain splice form (NCAM-140)  
C/Species: Mus musculus (house mouse)  
C/Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
C/Accession: A29673; S00844; S00384; A28281; A44290; S00383  
R/Barthels, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Pontec  
EMBO J. 6, 907-914, 1987  
A/Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000  
A/Reference number: A29673; MUID:87246524; PMID:3595563  
A/Accession: A29673  
A/Molecule type: mRNA  
A/Residues: 1-548, 'T', 550-571, 'T', 573-574, 'D', 576-588, 'MQPS', 593, 'S', 595-599, 'P', 601, 'L',  
A/Cross-references: UNIPROT:P13595; EMBL:Y00051; NID:G53342; PIDN:CAA68263.1; PID:G53343  
R/Santoni, M.J.; Barthels, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.; W  
Nucleic Acids Res. 15, 8621-8641, 1987  
A/Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse neur  
A/Reference number: S00844; MUID:88067687; PMID:3684567  
A/Accession: S00844  
A/Molecule type: mRNA  
A/Residues: 529-809, 1077-1115 <SAN>  
A/Cross-references: EMBL:X06328; NID:G53322; PIDN:CAA29641.1; PID:g817984  
R/Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.  
EMBO J. 7, 625-632, 1988  
A/Title: Differential splicing and alternative polyadenylation generates distinct NCAM t



A;Reference number: S00382; MUID:88283628; PMID:3396534  
A;Accession: S00384  
A;Molecule type: DNA  
A;Residues: 642-1115 <BAR>  
A;Cross-references: EMBL:X07195  
R;Barthelemy, D.; Vopper, G.; Wille, W.  
Nucleic Acids Res. 16, 4217-4225, 1988  
A;Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse,  
A;Reference number: A28281; MUID:88247737; PMID:2454455  
A;Accession: A28281  
A;Molecule type: mRNA  
A;Residues: 804-1081 <BA3>  
A;Cross-references: EMBL:X07244; NID:953321; PIDN:CAA30230.1; PID:929720  
R;Rougon, G.; Marshak, D.R.  
J. Biol. Chem. 261, 3396-3401, 1986  
A;Title: Structural and immunological characterization of the amino-terminal domain of m  
A;Reference number: A44290; MUID:86140120; PMID:3512556  
A;Accession: A44290  
A;Molecule type: protein  
A;Residues: 20-36 <ROU>  
C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol  
C;Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:JHMS  
C;Genetics:  
A;Gene: NCAM  
A;Map position: 9  
A;Introns: 643/3; 701/1; 770/2; 809/2; 1076/2  
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu  
C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-1115/Product: neural cell adhesion molecule, long domain splice form #status experi  
F;20-809,1077-1115/Product: neural cell adhesion molecule, short domain splice form #sta  
F;20-711/Domain: extracellular #status predicted <EXT>  
F;34-98/Domain: immunoglobulin homology <IMM1>  
F;132-191/Domain: immunoglobulin homology <IMM2>  
F;152-156/Region: heparin binding #status predicted  
F;161-165/Region: heparin binding #status predicted  
F;228-290/Domain: immunoglobulin homology <IMM3>  
F;262-272/Region: NCAM binding #status predicted  
F;323-388/Domain: immunoglobulin homology <IMM4>  
F;420-482/Domain: immunoglobulin homology <IMM5>  
F;519-596/Domain: fibronectin type III repeat homology <FN3A>  
F;625-685/Domain: fibronectin type III repeat homology <FN3B>  
F;712-729/Domain: transmembrane #status predicted <TM>  
F;730-1115/Domain: intracellular #status predicted <INT>  
F;41-96,139-189,235-288,330-386,427-480/Diulfide bonds: #status predicted  
F;222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.7%; Score 283.5; DB 1; Length 1115;  
Best Local Similarity 25.8%; Pred. No. 7.7e-13;  
Matches 75; Conservative 45; Mismatches 130; Indels 41; Gaps 7;  
QY 44 NVTVROGESATLRCTIDNRVTRVAVLNRSTILVAGNDKWLCDPRV-----LLSNTQ 95  
Db 222 NATANLQOSVTLVCDAGD-----FPEPTM-----SWTKDGEPIENEEDERSRSVS 268  
QY 96 TQYSIEIQNVVDVDEGPTCSVOTDNHPTKSRVHLIVQVSPKIVEISSDISINEGNNISL 155  
Db 269 DSSEVTRNVKDKDEAFYVCIENKAGEQDASHLKFAPKPKTYVNTQTAMLELEQVIL 328  
QY 156 TCIATGRPEPTVTR-----HISPKAVGFVSEDEYLEIQITREQSDYE 200  
Db 329 TCEASGDPIPSITWRTSTRNISSEEQDLGHMVVRSHRVSS---LTLKSIQYRDAGEYM 385  
QY 201 CSASNDVAAPVVRVKVTVNPPYVISEAKGTGVPVQKGTQCEASAVPSAEFQWYKDK 260  
Db 386 CTSANITGQD-SOSIDLEFQYAPKLGQFVAVYTWEGNQVNITCEVFAYPSATISWFRDQ 444  
QY 261 RLIEGK-KGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTASIML 310  
Db 445 LLPSSNVSNKIYNTPASVLEVTDPDSEDFGNVCTAVNRIQGESLEFLL 495

RESULT 11

JE0099  
neural cell adhesion molecule 1 - African clawed frog  
N;Alternate names: N-CAM 1  
C;Species: Xenopus laevis (African clawed frog)  
C;Date: 19-May-1998 #sequence\_revision 29-May-1998 #text\_change 09-Jul-2004  
C;Accession: JE0099  
R;Kudo, M.; Takayama, E.; Tadakuma, T.; Shiohawa, K.  
Biochem. Biophys. Res. Commun. 245, 127-132, 1998  
A;Title: Molecular cloning of ssd-form neural cell adhesion molecules (N-CAMs) as the ma  
A;Reference number: JE0099; MUID:98204770; PMID:9535795  
A;Accession: JE0099  
A;Molecule type: mRNA  
A;Residues: 1-725 <KUD>  
A;Cross-references: UNIPROT:O73633; DDBJ:AB08162; NID:G3116226; PIDN:BA025931.1; PID:G3  
A;Experimental source: heart  
C;Comment: This protein mediates and regulates various cell-cell interactions through bo  
C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu  
F;413-475/Domain: immunoglobulin homology <IMM>  
F;512-589/Domain: fibronectin type III repeat homology <3PR>  
Query Match 15.5%; Score 279.5; DB 2; Length 725;  
Best Local Similarity 27.9%; Pred. No. 8.7e-13;  
Matches 80; Conservative 50; Mismatches 120; Indels 37; Gaps 11;  
QY 44 NVTVROGESATLRCTIDN-RVTRVAVLNRSTILVAGNDKWLCDPRVLLSNTQTOYSIEI 102  
Db 219 NATAKVAESVLLSCDDAGFPDPPIISMLKGEPIEDGEEK-----ISFNEDQSEWTI 269  
QY 103 QNVVDVDEGPTCSVQTDNHPTKSRVHLIVQVSPKIVEISSDISINEGNNISLTCTIATGR 162  
Db 270 HHVEKDDEARYSCIANQAGEAEATILLKYVAKPKTYVENKTAV-ELDEITLTCEASGD 328  
QY 163 PEPVTW----RHISPKAV---GFVSEDEVLEITQGTRE-----QSGDYSCSASNDVAAP 210  
Db 329 PIPSITWRTAVRNISSEATLTDGHIIVVYKEHIRMALTKDIOYTDAGEYFCIASNPICVD 388  
QY 211 VVRVKVTVNPPYVISEAKGTGVPV-----GQKGTQCEASAVPSAEFQWYKDKRLIE 264  
Db 389 -MQMYFEVQYAPKI---RG---PVVYTWEGNVNITCEVFAHPRAVNTWFRDQGLPS 441  
QY 265 GK-KGVKVENRPFSLKLIFFNVSEHDYGNVTCVASKLGHNTASIML 310  
Db 442 SNFSNIKIYSGPTSSSLEVPDSEDFGNVCTAINTIGHEFSEFIL 488  
RESULT 12  
IJCHNL  
neural cell adhesion molecule long domain form precursor - chicken  
N;Alternate names: NCAM-180  
N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)  
C;Species: Gallus gallus (chicken)  
C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004  
C;Accession: A43613; B43613; A25435; B25435; A46550; S36950; A44369; A60852; S29668  
R;Cunningham, B.A.; Hemperly, J.J.; Murray, B.A.; Prediger, E.A.; Brackenbury, R.; Edelm  
Science 236, 799-806, 1987  
A;Title: Neural cell adhesion molecule: structure, immunoglobulin-like domains, cell sur  
A;Reference number: A43613; MUID:87206190; PMID:3576199  
A;Accession: A43613  
A;Molecule type: mRNA  
A;Residues: 1-175 <CU2>  
A;Cross-references: UNIPROT:P13590; GB:M15860  
A;Accession: B43613  
A;Molecule type: protein  
A;Residues: 20-44;120-127;202-221;320-342;399-415;640-659;822-828 <CUN>  
A;Note: Asn-222 probably binds carbohydrate; Asn-226 probably does not  
R;Hemperly, J.J.; Murray, B.A.; Edelman, G.M.; Cunningham, B.A.  
Proc. Natl. Acad. Sci. U.S.A. 83, 3037-3041, 1986  
A;Title: Sequence of a cDNA clone encoding the polylsialic acid-rich and cytoplasmic doma  
A;Reference number: A25435; MUID:86206089; PMID:3458261  
A;Accession: A25435  
A;Molecule type: mRNA  
A;Residues: 128-1091 <HEM>  
A;Cross-references: GB:M13210

```

Query Match      15.4%; Score 278.5; DB 2; Length 4162;
Best Local Similarity 27.3%; Pred. No. 9.5e-12;
Matches 78; Conservative 36; Mismatches 145; Indels 25; Gaps 7;

Qy 37 TFPKAMDNVTVROGESATLRECTI-DNRVTVAVLNRSTILYAGNDKWCLDPRVVLISNTQ 95
Db 3747 SFVKKPPFNVLSGENITFTTSIVKGSPLPEVKWFRGSIELAPGHK-----CNIT 3795
Qy 96 TQYSI---EIQNVDDYDEGPTTSCVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNN 152
Db 3796 LQDSVABLELFDVOPLOSQGYDTQVSNKGIKCTHLFVKPEAKFVKMKNVNDLSVEKGKN 3855
Qy 153 ISLTCTIATGRPEPTVTW-----RHISPRKAVGFVSEDEYLEIQGITREOSGDYECASIN 205
Db 3856 LILECTVTGTPISVTKWKGVLKHKSEKSIITTTETSAILEIPNSKLEDOQGYVSCHIE 3915
Qy 206 DVAAPVRRVKVTVNVYPY-ISEAKGTGVPVGQKGLQCEASAVPSAEFOWYKDDKRLIE 264
Db 3916 DSGQDNCHGA-ITILEPPYFVTPLEPVQVTVGDSASLQCVAGTPEMIVSWYKGDTKL-R 3973
Qy 265 GKGVKVKVENRPFSLKLIFFNVSEHDYGNVTCVASNKLGHNTASIML 310
Db 3974 GTATVKMHFNQVATLVFSQVSDSDSGEYICKVENTVGEATSSLL 4019

RESULT 14
IORTNC
neural cell adhesion molecule short domain form precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Alternate names: NCAM-140
C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004
C:Accession: S00846; B37795; I58136
F:Small, S.J.; Shull, G.E.; Santoni, M.J.; Akeson, R.
J. Cell Biol. 105, 2335-2345, 1987
A:Title: Identification of a cDNA clone that contains the complete coding sequence
A:Reference number: S00846; MUID:88059265; PMID:3680395
A:Accession: S00846
A:Molecule type: mRNA
A:Residues: 1-858 <SMA>
A:Cross-references: UNIPROT:P13596; EMBL:X06564

```

R;Small, S.J.; Akesson, R.  
 J. Cell Biol. 111, 2089-2096, 1990  
 A;Title: Expression of the unique NCAM VASE exon is independently regulated in distinct  
 A;Reference number: A37795; MUID:91035620; PMID:1699951  
 A;Accession: B37795  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 340-381 <SM2>  
 R;Small, S.J.; Haines, S.L.; Akesson, R.A.  
 Neuron 1, 1007-1017, 1988  
 A;Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is dev  
 A;Reference number: I58136; MUID:90166485; PMID:2483093  
 A;Accession: I58136  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 335-364 <RES>  
 A;Cross-references: GB:M32611; NID:g205643; PIDN:AAA41679.1; PID:g205644  
 C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol  
 C;Comment: Various forms of NCAM are produced by alternative splicing.  
 C;Genetics:  
 A;Gene: NCAM  
 C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu  
 C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-858/Product: neural cell adhesion molecule, short domain form #status predicted <MA  
 F;34-98/Domain: extracellular #status predicted <EXT>  
 F;132-191/Domain: immunoglobulin homology <IMM1>  
 F;152-156/Region: heparin binding #status predicted  
 F;161-165/Region: heparin binding #status predicted  
 F;228-290/Domain: immunoglobulin homology <IMM3>  
 F;263-272/Region: NCAM binding #status predicted  
 F;323-398/Domain: immunoglobulin homology <IMM4>  
 F;430-492/Domain: immunoglobulin homology <IMM5>  
 F;529-606/Domain: fibronectin type III repeat homology <FN3A>  
 F;635-695/Domain: fibronectin type III repeat homology <FN3B>  
 F;722-739/Domain: transmembrane #status predicted <TM>  
 F;740-858/Domain: intracellular #status predicted <INT>  
 F;41-96,139-189,235-288,330-396,437-490/Disulfide bonds: #status predicted  
 F;222,316,348,434,460,489/Binding site: carbohydrate (Asn) (covalent) #status predicted

C;Accession: S09600  
 R;Krieg, P.A.; Sakaguchi, D.S.; Kintner, C.R.  
 Nucleic Acids Res. 17, 10321-10335, 1989  
 A;Title: Primary structure and developmental expression of a large cytoplasmic domain fo  
 A;Reference number: S09600; MUID:90098871; PMID:2481269  
 A;Accession: S09600  
 A;Molecule type: mRNA  
 A;Residues: 1-1088 <KRI>  
 A;Cross-references: UNIPROT:P16170; EMBL:M25696; NID:g214609; PIDN:AAA49909.1; PID:g2146  
 A;Note: the authors translated the codon AAA for residue 970 as Leu  
 C;Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol  
 C;Comment: Several forms of NCAM are produced by alternative splicing.  
 C;Genetics:  
 A;Gene: NCAM  
 C;Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu  
 C;Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; si  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-1088/Product: neural cell adhesion molecule, long domain form #status predicted <LD  
 F;20-803,1050-1088/Product: neural cell adhesion molecule, short domain form #status pre  
 F;20-705/Domain: extracellular #status predicted <EXT>  
 F;34-95/Domain: immunoglobulin homology <IMM1>  
 F;129-188/Domain: immunoglobulin homology <IMM2>  
 F;149-153/Region: heparin binding #status predicted  
 F;158-162/Region: heparin binding #status predicted  
 F;225-284/Domain: immunoglobulin homology <IMM3>  
 F;317-381/Domain: immunoglobulin homology <IMM4>  
 F;413-475/Domain: immunoglobulin homology <IMM5>  
 F;512-589/Domain: fibronectin type III repeat homology <FN3A>  
 F;618-679/Domain: fibronectin type III repeat homology <FN3B>  
 F;706-723/Domain: transmembrane #status predicted <TM>  
 F;724-1088/Domain: intracellular #status predicted <INT>  
 F;41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted  
 F;219,310,341,417,443,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.4%; Score 277.5; DB 1; Length 1088;  
 Best Local Similarity 27.9%; Pred. No. 2.1e-12;  
 Matches 80; Conservative 49; Mismatches 121; Indels 37; Gaps 11;  
 QY 44 NVTVRQGESATLCTIDN-RVTRVAVLNRSITLYAGNDKWCLDPRVLLSNTQTSIEI 102  
 DB 219 NATANNAESVVLSCDADGFPDPFISWLKKEPIEDGEK-----ISFNEDQSEMTI 269  
 QY 103 QNVVDVDEGPTCSVQTDNHPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCTATGR 162  
 DB 270 HHVEKDDAEYSKIANNQAGEAETILLKYAKPKITYVENKTAV-ELDEITITCEASGD 328  
 QY 163 PEPTVTW----RHISPKAV---GFVSEDEYLEIQITRE-----QSGDYECASNDVAAAP 210  
 DB 329 PIPSITWRTAVRNISSEATTLGDHIVVKEHIRMALTLKDIQYTDAGEYFCIASNPIGVD 388  
 QY 211 VVRRVKVTNYPPISEAKGTGPV-----GQKGTLOCEASAVPSAEFQWYKDKKELIE 264  
 DB 389 -MQAMTFEYQYAPKI---RG---PVVYTWEGPNVITCEVFAHPRAAAVTFRFGQLLPS 441  
 QY 265 GK-KGVKVENRPFLSKLIFNVSEHDYGNVTCVASKLGHNTASIML 310  
 DB 442 SNPSNKKIYSGPTSSSSLEVPDSEDFGNVNTAINTIGHEPSEFIL 488

Search completed: October 19, 2005, 16:28:54  
 Job time : 61 secs

RESULT 15  
 LUXNL  
 neural cell adhesion molecule long domain form precursor - African clawed frog  
 N;Alternate names: NCAM-180  
 N;Contains: neural cell adhesion molecule, short domain form (NCAM-140)  
 C;Species: Xenopus laevis (African clawed frog)  
 C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004

**THIS PAGE BLANK (USPTO)**

GenCore version 5.1.6  
OM protein - protein search, using sw model  
Run on: October 19, 2005, 16:27:52 ; Search time 168 Seconds  
(without alignments)  
791.938 Million cell updates/sec

Title: US-09-978-544A-523  
Perfect score: 1806  
Sequence: 1 MKTIQPMHNSISWAIFTGL.....RRAGCVMLPLVLVHLLK 344  
Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5  
Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 2105692  
Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1500 summaries  
Database :  
A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAV57601	standard; protein; 344 AA.				
DE	Human protein SEQ ID NO:1.					
PN	WO9598668-A1.					
PD	18-NOV-1999.					
PA	(ONCY ) ONO PHARM CO LTD.					
Query Match	100.0%;	Score 1806;	DB 3;	Length 344;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;				
RESULT 2						
ID	AA44329	standard; protein; 344 AA.				
DE	Human PRO337 protein sequence SEQ ID NO:523.					
PN	WO200053756-A2.					
PD	14-SEP-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1806;	DB 3;	Length 344;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;				
RESULT 3						
ID	AAB31204	standard; protein; 344 AA.				
DE	Amino acid sequence of human polypeptide PRO337.					
PN	WO200077037-A2.					
PD	21-DEC-2000.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1806;	DB 3;	Length 344;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;				
RESULT 4						
ID	AAU12359	standard; protein; 344 AA.				
DE	Human PRO337 polypeptide sequence.					
PN	WO200140466-A2.					
PD	07-JUN-2001.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1806;	DB 4;	Length 344;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;				
RESULT 5						
ID	AAU83654	standard; protein; 344 AA.				
DE	Human PRO protein, Seq ID No 126.					
PN	WO200208288-A2.					
PD	31-JAN-2002.					
PA	(GETH ) GENENTECH INC.					
Query Match	100.0%;	Score 1806;	DB 5;	Length 344;		
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;				
RESULT 6						
ID	ABB84844	standard; protein; 344 AA.				

Human PRO337 protein sequence SEQ ID NO:56.  
WO20020690-A2.  
03-JAN-2002.  
(GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 5; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 7  
ID ABB95450 standard; protein; 344 AA.  
DE Human angiogenesis related protein PRO337 SEQ ID NO: 56.  
PN WO200208284-A2.  
PD 31-JAN-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 5; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 8  
ID ABO17803 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003032156-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 9  
ID ASU80801 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003036635-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 10  
ID ABO25175 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003040014-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 11  
ID ABO25275 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003050239-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 12  
ID ABO33767 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 13  
ID ASU81057 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003004311-A1.

PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 14  
ID ABU72281 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2002192706-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 15  
ID ABU6757 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003036180-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 16  
ID ABU67293 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003032063-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 17  
ID ABU84961 standard; protein; 344 AA.  
DE Human secreted and transmembrane PRO polypeptide #37.  
PN US2002177553-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 18  
ID ABUS938 standard; protein; 344 AA.  
DE Novel secreted and transmembrane protein PRO337.  
PN US2003017563-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 19  
ID ABU61159 standard; protein; 344 AA.  
DE Human PRO337 polypeptide.  
PN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 20  
ID ABO25028 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein (PRO) #188.  
PN US2003036179-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 21  
ID ABU72061 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2002177165-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 22  
ID ABU67162 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003032062-A1.  
PD 13-FEB-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 23  
ID ABU80428 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein PRO337.  
PN US2003004102-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 24  
ID ABU82110 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 25  
ID ABU67033 standard; protein; 344 AA.  
DE Human secreted/transmembrane, PRO, protein SEQ ID 376.  
PN US2003032155-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 26  
ID ABU79804 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein PRO337.  
PN US2003032057-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 27  
ID ADA45895 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003022328-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 28  
ID ADA76326 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003073212-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 29  
ID ABJ72290 standard; protein; 344 AA.  
DE Human PRO337 protein.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 30  
ID ADA18976 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003054517-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 31  
ID ADA61599 standard; protein; 344 AA.  
DE Homo sapiens.  
PN US2003049816-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 32  
ID ADB19384 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003068796-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 33  
ID ADB27925 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003082704-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 34  
ID ADA86404 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003082711-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 35  
ID ADB15968 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003087350-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 36  
ID ADA47754 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003073215-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 37  
ID ADA67549 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 38  
ID ADB30556 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 39  
ID ADA85852 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 40  
ID ADA97064 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;

Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 41  
ID ADA79368 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 42  
ID ADA87507 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 43  
ID ADB16709 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 44  
ID ADA91801 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 45  
ID ADB14864 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 46  
ID ADA25062 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003050241-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 47  
ID ADA47276 standard; protein; 344 AA.  
DE Human secreted/transmembrane polypeptide PRO337.  
PN US2003044844-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 48  
ID ADB18825 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 49  
ID ADA94040 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 6; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;

```
RESULT 50
ID ADB19936 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082691-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 51
ID ADB13248 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082710-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 52
ID ABO43336 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003044945-A1.
PD 06-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 53
ID ABO19730 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003050240-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 54
ID ADA12723 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO337.
PN US2003055216-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 55
ID ADA74502 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068798-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 56
ID ADB24735 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077713-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 57
ID ADA82259 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082701-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 58
ID ADA75222 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073216-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 59
ID ADB31108 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082695-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 60
ID ADA84748 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082708-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 61
ID ADB30004 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073214-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 62
ID ADA80532 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082761-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 63
ID ADA75774 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082703-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 64
ID ADA46999 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003073210-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 65
ID ADB25295 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077715-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 66
ID ADA93471 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077721-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 67
ID ADB26821 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003092147-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 68
ID ADB31108 standard; protein; 344 AA.
```



```
DE Human PRO polypeptide #188.
PN US2003096386-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 69
ID ABJ72418 standard; protein; 344 AA.
DE Human PRO337 protein.
PN US2003027988-A1.
PD 06-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 70
ID ADA61036 standard; protein; 344 AA.
DE Homo sapiens.
PN US2003049817-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 71
ID ADB24183 standard; protein; 344 AA.
DE Human PRO polypeptide SEQ ID NO 376.
PN US2003077714-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 72
ID ADA96512 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082690-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 73
ID ADA81084 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082702-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 74
ID ADA95960 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082759-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 75
ID ADB26269 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082760-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 76
ID ADB21754 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082765-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 77
ID ABO34313 standard; protein; 344 AA.
DE Human secreted/transmembrane polypeptide PRO 337.
PN US2003059909-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 78
ID ABO19621 standard; protein; 344 AA.
DE Novel human secreted and transmembrane polypeptide #89.
PN US2003049633-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 6; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 79
ID ADA77533 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003068797-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 80
ID ADB18273 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003077710-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 81
ID ADA86956 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082709-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 82
ID ADA88059 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003082700-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 83
ID ADA46447 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003054516-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 84
ID ADB28477 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082699-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 85
ID ADB29029 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003082706-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 86
ID ADA76981 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003059909-A1.
PD 27-MAR-2003.
```

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 87  
ID ADA8611 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003073213-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 88  
ID ADA97616 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003082686-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 89  
ID ADB27373 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003022239-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 90  
ID ADB22306 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003087344-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 91  
ID ABO19862 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein PRO337.  
PN US2003044902-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 92  
ID ABJ72120 standard; protein; 344 AA.  
DE Human membrane bound receptor/protein PRO337 amino acid sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 93  
ID ADA6997 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003068793-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 94  
ID ADB22858 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003077711-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 95  
ID ADB23631 standard; protein; 344 AA.  
DE Human PRO polypeptide SEQ ID NO 376.  
PN US2003077712-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;

RESULT 96  
ID ADA92353 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003082712-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 97  
ID ADB15416 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003087352-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 98  
ID ADB83616 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 99  
ID ADB80722 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 100  
ID ADB73263 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 101  
ID ADB38668 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003082766-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 102  
ID ADB78345 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 103  
ID ADB38116 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003087347-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 104  
ID ADB66588 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 105  
ID ADB66588 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003082689-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;

ID ADB84993 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 106  
ID ADB89668 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003082698-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 107  
ID ADB90400 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003082762-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 108  
ID ADB9501 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003082764-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 109  
ID ADB78099 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 110  
ID ADB74029 standard; protein; 344 AA.  
DE Human PRO polypeptide #89.  
PN US2003045462-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 111  
ID ADB87165 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 112  
ID ADB84747 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 113  
ID ADB47124 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003082687-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 114  
ID ADB83862 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO337.  
PN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 115  
ID ADB86731 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003082697-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 116  
ID ADB73017 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003092887-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 117  
ID ADB67745 standard; protein; 344 AA.  
DE Human PRO polypeptide #89.  
PN US2003083248-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 118  
ID ADB77336 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003082696-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 119  
ID ADB34493 standard; protein; 344 AA.  
DE Human PRO polypeptide SEQ ID NO 376.  
PN US2003077717-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 120  
ID ADB35597 standard; protein; 344 AA.  
DE Human PRO polypeptide SEQ ID NO 376.  
PN US2003077719-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 121  
ID ADB33941 standard; protein; 344 AA.  
DE Human PRO polypeptide SEQ ID NO 376.  
PN US2003077716-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 122  
ID ADB35045 standard; protein; 344 AA.  
DE Human PRO polypeptide SEQ ID NO 376.  
PN US2003077718-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 123  
ID ADB36149 standard; protein; 344 AA.  
DE Human PRO polypeptide SEQ ID NO 376.

```
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 124
  ID ADB46544 standard; protein; 344 AA.
  DE Novel human secreted and transmembrane protein PRO337.
  PN US2003082692-A1.
  PD 01-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 125
  ID ADC44171 standard; protein; 344 AA.
  DE Human secreted/transmembrane protein, PRO337.
  PN US2003054986-A1.
  PD 20-MAR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 126
  ID ADC61931 standard; protein; 344 AA.
  DE Human secreted/transmembrane protein, PRO337.
  PN US2003049684-A1.
  PD 13-MAR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 127
  ID ADC63895 standard; protein; 344 AA.
  DE Human secreted/transmembrane protein, PRO337.
  PN US2003054405-A1.
  PD 20-MAR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 128
  ID ADC66995 standard; protein; 344 AA.
  DE Human secreted/transmembrane protein, PRO337.
  PN US2003060406-A1.
  PD 27-MAR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 129
  ID ADC69119 standard; protein; 344 AA.
  DE Human secreted/transmembrane protein, PRO337.
  PN US2003064407-A1.
  PD 03-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 130
  ID ADC63179 standard; protein; 344 AA.
  DE Human secreted/transmembrane protein, PRO337.
  PN US2003068648-A1.
  PD 10-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 131
  ID ADC68244 standard; protein; 344 AA.
  DE Human secreted/transmembrane protein, PRO337.
  PN US2003069178-A1.
  PD 10-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 132
  ID ADC41564 standard; protein; 344 AA.
  DE Human secreted/transmembrane protein, PRO337.
  PN US2003072745-A1.

PN 17-APR-2003.
PD (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 133
  ID ADC67619 standard; protein; 344 AA.
  DE Human secreted/transmembrane protein, PRO337.
  PN US2003073131-A1.
  PD 17-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 134
  ID ADC62555 standard; protein; 344 AA.
  DE Human secreted/transmembrane protein, PRO337.
  PN US2003073624-A1.
  PD 17-APR-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 135
  ID ADC36855 standard; protein; 344 AA.
  DE Human PRO polypeptide #63.
  PN US2003088065-A1.
  PD 08-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 136
  ID ADC42188 standard; protein; 344 AA.
  DE Human secreted/transmembrane protein, PRO337.
  PN US2003104998-A1.
  PD 05-JUN-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 137
  ID ADC21845 standard; protein; 344 AA.
  DE Human PRO polypeptide #63.
  PN US2003096969-A1.
  PD 22-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 138
  ID ADC50417 standard; protein; 344 AA.
  DE Novel human secreted and transmembrane protein PRO337.
  PN US2003092106-A1.
  PD 15-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 139
  ID ADC71964 standard; protein; 344 AA.
  DE Novel human secreted and transmembrane protein PRO337.
  PN US2003092107-A1.
  PD 15-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 140
  ID ADC59943 standard; protein; 344 AA.
  DE Novel human secreted and transmembrane protein PRO337.
  PN US2003092105-A1.
  PD 15-MAY-2003.
  PA (GETH ) GENENTECH INC.
  Query Match
  Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
  RESULT 141
  ID ADC49876 standard; protein; 344 AA.
  DE Novel human secreted and transmembrane protein PRO337.
  PN US2003088064-A1.
  PD 08-MAY-2003.
```

PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 142  
ID ADC49075 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003088070-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 143  
ID ADC49592 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003088071-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 144  
ID ADC47453 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003088072-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 145  
ID ADC52950 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein Seq ID376.  
FN US2003087365-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 146  
ID ADC57304 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein Seq ID376.  
FN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 147  
ID ADC60495 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 148  
ID ADC50970 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 149  
ID ADC65497 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
FN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 150  
ID ADC54595 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein Seq ID376.  
FN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.

Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 151  
ID ADC53556 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein Seq ID376.  
FN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 152  
ID ADC59079 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein Seq ID376.  
FN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 153  
ID ADC55957 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein Seq ID376.  
FN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 154  
ID ADC58527 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein Seq ID376.  
FN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 155  
ID ADC47198 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003105288-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 156  
ID ADD03201 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 157  
ID ADC90193 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 158  
ID ADC69612 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
FN US2003194770-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 159  
ID ADC48501 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
FN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;  
RESULT 160  
ID ADC54595 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein Seq ID376.  
FN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.

```
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 160
ID ADI10030 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194776-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 161
ID ADC78073 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096972-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 162
ID ADD04605 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087354-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 163
ID ADP06308 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003073816-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 164
ID ADC80561 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092103-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 165
ID ADI11068 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194774-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 166
ID ADI10345 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 167
ID ADC47949 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194771-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 168
ID ADC77827 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003088066-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 169
ID ADC80009 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087358-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 170
ID ADD11305 standard; protein; 344 AA.
DE Human secreted/transmembrane PRO polypeptide #28.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 171
ID ADD09478 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194775-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 172
ID ADD50790 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105291-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 173
ID ADD41191 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003203438-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 174
ID ADD52330 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194769-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 175
ID ADD51036 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003105290-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 176
ID ADD53070 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194792-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 177
ID ADD53622 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003203437-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 178
```

ID ADD37098 standard; protein; 344 AA.  
DE Human secreted/transmembrane PRO polypeptide #28.  
PN US2003105012-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 179  
ID ADD511778 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 180  
ID ADD02577 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 181  
ID ADD050517 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003096971-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 182  
ID ADD02011 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 183  
ID ADD54193 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 184  
ID ADD50271 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003096970-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 185  
ID ADD51282 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003105289-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 186  
ID ADE49557 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 187  
ID ADD92510 standard; protein; 344 AA.

DE Human PRO polypeptide #188.  
PN US2003199030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 188  
ID ADD91406 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003199055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 189  
ID ADE04020 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003199057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 190  
ID ADE32317 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 191  
ID ADE22249 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003199056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 192  
ID ADD79473 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 193  
ID ADE35611 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 194  
ID ADE16725 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 195  
ID ADE16725 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 196  
ID ADD73340 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003203436-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 197  
ID ADE42009 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.



```
PN US2003194772-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 197
ID ADE17826 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199023-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 198
ID ADD91958 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199053-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 199
ID ADE33421 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194767-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 200
ID ADE33973 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194791-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 201
ID ADD80025 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207417-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 202
ID ADD93062 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003194768-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 203
ID ADD72698 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003194781-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 204
ID ADE19482 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199025-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 205
ID ADE18930 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199026-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 206
ID ADE43126 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199033-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 207
ID ADD95915 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199059-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 208
ID ADE22801 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199064-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 209
ID ADD78919 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003203429-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 210
ID ADE32869 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003194766-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 211
ID ADE42561 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199032-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 212
ID ADE17349 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003203433-A1.
PD 30-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 213
ID ADD80577 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207418-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1806; DB 7; Length 344;
RESULT 214
ID ADD89605 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199028-A1.
PD 23-OCT-2003.
```

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 215  
ID ADE40899 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003199031-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 216  
ID ADE04688 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003199034-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 217  
ID ADE92817 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003194777-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 218  
ID ADF47363 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003195333-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 219  
ID ADG21526 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207355-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 220  
ID ADG23167 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207384-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 221  
ID ADF97502 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003207370-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 222  
ID ADG80566 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003207373-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 223  
ID ADG53120 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003216561-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.

Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 224  
ID ADG60440 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003206915-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 225  
ID ADG80014 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003207372-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 226  
ID ADG63785 standard; protein; 344 AA.  
DE Human secreted/transmembrane polypeptide PRO337.  
PN US2003170721-A1.  
PD 11-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 227  
ID ADH53306 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207381-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 228  
ID ADH55858 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207379-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 229  
ID ADI61200 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003077700-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 230  
ID ADI64077 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 231  
ID ADI65026 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 232  
ID ADI63525 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 7; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 233  
ID ADI63120 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003216561-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.

```
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 233
ID ADH81939 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207388-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 234
ID ADH81387 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207377-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 235
ID ADH82556 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087355-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 236
ID ADN15955 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087353-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 237
ID ADN16584 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087385-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 238
ID ADN15403 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087356-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 239
ID ADN14851 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003087357-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 7; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 240
ID ADC48829 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092888-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 241
ID ADC81113 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003092115-A1.
PD 15-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 242
ID ADE21000 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 243
ID ADE05844 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 244
ID ADD76561 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003100087-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 245
ID ADD75073 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 246
ID ADD75819 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 247
ID ADD85051 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 248
ID ADD86877 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 249
ID ADE20754 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 250
ID ADE39051 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 251
```

ID ADD87925 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 252  
ID ADD86329 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 253  
ID ADE05598 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003100727-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 254  
ID ADD73583 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003100711-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 255  
ID ADE75777 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003211571-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 256  
ID ADE48857 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003104536-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 257  
ID ADD78423 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003100737-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 258  
ID ADE41306 standard; protein; 344 AA.  
DE Human secreted/transmembrane PRO polypeptide #28.  
PN US2003100497-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 259  
ID ADE23353 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 260  
ID ADE21246 standard; protein; 344 AA.

DE Novel human secreted and transmembrane protein PRO337.  
PN US2003100736-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 261  
ID ADD77361 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003100732-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 262  
ID ADE20508 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003100733-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 263  
ID ADD75573 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003100064-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 264  
ID ADD74089 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003100708-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 265  
ID ADD74335 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003100709-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 266  
ID ADD76065 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003100718-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 267  
ID ADD85557 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003100721-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 268  
ID ADE23905 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 269  
ID ADE24548 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.

PN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 270  
ID ADD87373 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 271  
ID ADE05106 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003100726-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 272  
ID ADD75319 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003100714-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 273  
ID ADD76863 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003100715-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 274  
ID ADD86631 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003100719-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 275  
ID ADE89239 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 276  
ID ADE41199 standard; protein; 344 AA.  
DE Human secreted/transmembrane polypeptide PRO337.  
PN US2003104558-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 277  
ID AD78099 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003100731-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 278  
ID ADE18378 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003194794-A1.

PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 279  
ID ADE86687 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 280  
ID ADE89958 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003130181-A1.  
PD 10-JUL-2003.  
PA (ASHK/) ASHKENAZI A J.  
PA (BAKE/) BAKER K P.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GIRM/) GIRMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (KUOS/) KUO S S.  
PA (NAPI/) NAPIER M A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (SHEL/) SHELTON D L.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 281  
ID ADD77607 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003100729-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 282  
ID ADD77853 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003100730-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 283  
ID ADE85311 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003100725-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 284  
ID ADD73843 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.

PN US2003100710-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 285  
ID ADD74581 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003100713-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 286  
ID ADD77109 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003100716-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 287  
ID ADD85803 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003100720-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 288  
ID ADE05352 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003100723-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 289  
ID ADD74827 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003100724-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 290  
ID ADF61598 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003195345-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 291  
ID ADF40290 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003198994-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 292  
ID ADF46086 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003195148-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 293  
ID ADE94707 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003199027-A1.

PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 294  
ID ADE91118 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 295  
ID ADE95259 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 296  
ID ADE93369 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 297  
ID ADF24482 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003204055-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 298  
ID ADF40914 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003199021-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 299  
ID ADF23858 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003203402-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 300  
ID ADF33841 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003194780-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 301  
ID ADF34950 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 302  
ID ADF27308 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003199436-A1.  
PD 23-OCT-2003.

```
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 303
ID ADF27944 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199437-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 304
ID ADE92265 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003199051-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 305
ID ADE90566 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003199063-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 306
ID ADF41538 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199435-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 307
ID ADF33217 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003211091-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 308
ID ADF25583 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003211092-A1.
PD 13-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 309
ID ADF26684 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003199674-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 310
ID ADF34473 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003194410-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 311
ID ADF46710 standard; protein; 344 AA.
DE Human secreted/transmembrane protein, PRO337.
PN US2003195344-A1.
PD 16-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 312
ID ADE91713 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003199058-A1.
PD 23-OCT-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 313
ID ADG05639 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003096959-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 314
ID ADG27193 standard; protein; 344 AA.
DE Human PRO polypeptide #63.
PN US2003096962-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 315
ID ADG02292 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207352-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 316
ID ADG22078 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207360-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 317
ID ADG20148 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207376-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 318
ID ADF98054 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003207422-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 319
ID ADG24271 standard; protein; 344 AA.
DE Novel human secreted and transmembrane protein PRO337.
PN US2003207426-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
Best Local Similarity 100.0%; Pred. No. 4.3e-147;
RESULT 320
ID ADF98625 standard; protein; 344 AA.
DE Human PRO polypeptide #188.
PN US2003208055-A1.
PD 06-NOV-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1806; DB 8; Length 344;
```



RESULT 330  
ID ADG12035 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003096963-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 331  
ID ADF96950 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
FN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 332  
ID ADS06135 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
FN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 333  
ID ADG23719 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 334  
ID ADG04008 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
FN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 335  
ID ADG24909 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 336  
ID ADF94592 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003096964-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 337  
ID ADG07206 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 338  
ID ADG07758 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 339  
ID ADG07758 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 339

ID ADG06688 standard; protein; 344 AA.  
DE Human PRO polypeptide #63.  
PN US2003096966-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 340  
ID ADG55253 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 341  
ID ADG60917 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 342  
ID ADG62021 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 343  
ID ADG82222 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 344  
ID ADG57461 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 345  
ID ADG56909 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 346  
ID ADG5805 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 347  
ID ADG58565 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 348  
ID ADG70931 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207419-A1.

DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207420-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 349  
ID ADH39032 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003096965-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 350  
ID ADG58013 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 351  
ID ADG53597 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 352  
ID ADG71483 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 353  
ID ADG50696 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2003207803-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 354  
ID ADG81670 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 355  
ID ADH30632 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 356  
ID ADG63634 standard; protein; 344 AA.  
DE Human secreted/transmembrane polypeptide PRO337.  
PN US2003180796-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 357  
ID ADH11999 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207419-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 358  
ID ADG50072 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
FN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 359  
ID ADG51944 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
FN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 360  
ID ADG52421 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 361  
ID ADG54149 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 362  
ID ADG49448 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
FN US2003216305-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 363  
ID ADG81118 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
FN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 364  
ID ADG56357 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 365  
ID ADH12623 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 366  
ID ADG48824 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
FN US2003216560-A1.  
PD 20-NOV-2003.

PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 367  
ID ADG61469 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 368  
ID ADH28556 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
FN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 369  
ID ADG54701 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 370  
ID ADG59741 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 371  
ID ADG51320 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
FN US2004005312-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 372  
ID ADH43489 standard; protein; 344 AA.  
DE Human PRO polypeptide #28.  
FN US2003224984-A1.  
PD 04-DEC-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 373  
ID ADG59264 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
FN US2004005657-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 374  
ID ADG34122 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
FN US2004006206-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 375  
ID ADG62720 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
FN US2004006219-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.

Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 376				
ID ADI1165 standard; protein; 344 AA.				
DE Human PRO polypeptide #188.				
PN US2003207361-A1.				
PD 06-NOV-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 377				
ID ADI33592 standard; protein; 344 AA.				
DE Human PRO polypeptide #63.				
PN US2003096960-A1.				
PD 22-MAY-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 378				
ID ADH69686 standard; protein; 344 AA.				
DE Human PRO polypeptide #63.				
PN US2004019183-A1.				
PD 29-JAN-2004.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 379				
ID ADH25745 standard; protein; 344 AA.				
DE Human PRO337 protein SEQ ID NO:523.				
PN EPI386931-A1.				
PD 04-FEB-2004.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 380				
ID ADG09908 standard; protein; 344 AA.				
DE Novel human secreted and transmembrane protein PRO337.				
PN US2004009548-A1.				
PD 15-JAN-2004.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 381				
ID ADI11379 standard; protein; 344 AA.				
DE Novel human secreted and transmembrane protein PRO337.				
PN US2003207382-A1.				
PD 06-NOV-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 382				
ID AUG09256 standard; protein; 344 AA.				
DE Novel human secreted and transmembrane protein PRO337.				
PN US2004009547-A1.				
PD 15-JAN-2004.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 383				
ID ADI14711 standard; protein; 344 AA.				
DE Novel human secreted and transmembrane protein PRO337.				
PN US2003207383-A1.				
PD 06-NOV-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 384				
ID ADI29847 standard; protein; 344 AA.				
DE Novel human secreted and transmembrane protein PRO337.				
PN US2003096961-A1.				
PD 22-MAY-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 385				
ID ADI18306 standard; protein; 344 AA.				
DE Novel human secreted and transmembrane protein PRO337.				
PN US2003207349-A1.				
PD 06-NOV-2003.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 386				
ID ADM27244 standard; protein; 344 AA.				
DE Novel human secreted and transmembrane protein PRO337.				
PN US2004044179-A1.				
PD 04-MAR-2004.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;	Pred. No. 4.3e-147;		
RESULT 387				
ID ADJ63587 standard; protein; 344 AA.				
DE Novel human secreted and transmembrane protein PRO337.				
PN US2004039164-A1.				
PD 26-FEB-2004.				
PA (GETH ) GENENTECH INC.				
Query Match	100.0%;	Score 1806;	DB 8;	Length 344;
Best Local Similarity	100.0%;</			

RESULT 394  
ID ADL07356 standard; protein; 344 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2004063921-A1.  
PD 01-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 395  
ID ADM42464 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 396  
ID ADM28326 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 397  
ID ADI95808 standard; protein; 344 AA.  
DE Human PRO polypeptide #188.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 398  
ID ADI96360 standard; protein; 344 AA.  
DE Novel human secreted and transmembrane protein PRO337.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 399  
ID AAM40499 standard; protein; 355 AA.  
DE Human polypeptide SEQ ID NO 5430.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 4; Length 355;  
Best Local Similarity 100.0%; Pred. No. 4.5e-147;  
RESULT 400  
ID ADI21580 standard; protein; 355 AA.  
DE Novel human polypeptide #59.  
PN WO2003025148-A2.  
PD 27-MAR-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 7; Length 355;  
Best Local Similarity 100.0%; Pred. No. 4.5e-147;  
RESULT 401  
ID AAB19722 standard; protein; 344 AA.  
DE Human SECK Clone 11753149.0.37-encoded protein.  
PN WO200061754-A2.  
PD 19-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 99.6%; Score 1799; DB 3; Length 344;  
Best Local Similarity 99.7%; Pred. No. 1.7e-146;  
RESULT 402  
ID AAB19721 standard; protein; 344 AA.  
DE Human SECK Clone 11753149.0.6-encoded protein.  
PN WO200061754-A2.  
PD 19-OCT-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 99.6%; Score 1799; DB 3; Length 344;  
Best Local Similarity 99.7%; Pred. No. 1.7e-146;  
RESULT 403  
ID ADI35770 standard; protein; 355 AA.  
DE Human secreted/transmembrane protein, PRO337.  
PN US2004063921-A1.  
PD 01-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 100.0%; Score 1806; DB 8; Length 344;  
Best Local Similarity 100.0%; Pred. No. 4.3e-147;  
RESULT 404  
ID ADI18289 standard; protein; 344 AA.  
DE Human molecule (MOL) protein MOL10.  
PN WO2003003984-A2.  
PD 16-JAN-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match  
Best Local Similarity 99.6%; Score 1799; DB 7; Length 344;  
Best Local Similarity 99.7%; Pred. No. 1.7e-146;  
RESULT 405  
ID AAY41773 standard; protein; 343 AA.  
DE Human PRO337 protein sequence.  
PN WO9946281-A2.  
PD 16-SEP-1999.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 99.2%; Score 1791.5; DB 2; Length 343;  
Best Local Similarity 99.7%; Pred. No. 7.7e-146;  
RESULT 406  
ID AAM38713 standard; protein; 344 AA.  
DE Human polypeptide SEQ ID NO 1858.  
PN WO200153312-A1.  
PD 26-JUL-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match  
Best Local Similarity 92.2%; Score 1665.5; DB 4; Length 344;  
Best Local Similarity 95.2%; Pred. No. 5.7e-135;  
RESULT 407  
ID AB320227 standard; protein; 344 AA.  
DE Human IG gene related protein SEQ ID NO 50.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match  
Best Local Similarity 92.2%; Score 1665.5; DB 6; Length 344;  
Best Local Similarity 95.2%; Pred. No. 5.7e-135;  
RESULT 408  
ID ABU56719 standard; protein; 344 AA.  
DE Lung cancer-associated polypeptide #312.  
PN WO200286443-A2.  
PD 31-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 92.2%; Score 1665.5; DB 6; Length 344;  
Best Local Similarity 95.2%; Pred. No. 5.7e-135;  
RESULT 409  
ID ADG63209 standard; protein; 344 AA.  
DE Human neurotrophin protein.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match  
Best Local Similarity 92.2%; Score 1665.5; DB 7; Length 344;  
Best Local Similarity 95.2%; Pred. No. 5.7e-135;  
RESULT 410  
ID ADN39138 standard; protein; 344 AA.  
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:456.  
PN WO2003042661-A2.  
PD 22-MAY-2003.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match  
Best Local Similarity 92.2%; Score 1665.5; DB 7; Length 344;  
Best Local Similarity 95.2%; Pred. No. 5.7e-135;  
RESULT 411  
ID ADG63211 standard; protein; 355 AA.  
DE Human neurotrophin protein +33bp isoform.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match  
Best Local Similarity 91.4%; Score 1650; DB 7; Length 355;  
Best Local Similarity 92.2%; Pred. No. 1.3e-133;  
RESULT 412  
ID ADI35770 standard; protein; 355 AA.

DE Human neurotrophin.  
PN US2003100485-A1.  
PD 29-MAY-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 91.4%; Score 1650; DB 7; Length 355;  
Best Local Similarity 92.2%; Pred. No. 1.3e-133;  
RESULT 413  
ID ADG63213 standard; protein; 367 AA.  
DE Human neurotrophin protein +69bp isoform.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match 91.0%; Score 1644; DB 7; Length 367;  
Best Local Similarity 89.1%; Pred. No. 4.5e-133;  
RESULT 414  
ID AAU79205 standard; protein; 381 AA.  
DE Human Kruppel associated DNA binding protein 42.  
PN WO200183541-A1.  
PD 08-NOV-2001.  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
Query Match 91.0%; Score 1643; DB 5; Length 381;  
Best Local Similarity 98.7%; Pred. No. 5.7e-133;  
RESULT 415  
ID AAY57602 standard; protein; 313 AA.  
DE Human protein SEQ ID NO:4.  
PN WO9958668-A1.  
PD 18-NOV-1999.  
PA (ONVOY ) ONO PHARM CO LTD.  
Query Match 90.9%; Score 1642; DB 3; Length 313;  
Best Local Similarity 100.0%; Pred. No. 5.3e-133;  
RESULT 416  
ID ADI35772 standard; protein; 344 AA.  
DE Rat neurotrophin.  
PN US2003100485-A1.  
PD 29-MAY-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 90.8%; Score 1639.5; DB 7; Length 344;  
Best Local Similarity 92.9%; Pred. No. 1e-132;  
RESULT 417  
ID ADG63215 standard; protein; 376 AA.  
DE Human neurotrophin protein +108bp isoform.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match 90.8%; Score 1639.5; DB 7; Length 376;  
Best Local Similarity 87.0%; Pred. No. 1.1e-132;  
RESULT 418  
ID ADE07928 standard; protein; 338 AA.  
DE Novel protein (useful for identifying genetic disorders) #83.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 71.7%; Score 1295.5; DB 7; Length 338;  
Best Local Similarity 71.6%; Pred. No. 4.6e-103;  
RESULT 419  
ID AO47380 standard; protein; 250 AA.  
DE Human neurotrophin-like protein-related rat neurotrophin protein SeqID15.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO.  
Query Match 71.7%; Score 1295; DB 8; Length 250;  
Best Local Similarity 97.6%; Pred. No. 3.3e-103;  
RESULT 420  
ID ABJ20236 standard; protein; 345 AA.  
DE Human IG gene related protein SEQ ID NO 59.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 70.2%; Score 1268; DB 6; Length 345;  
Best Local Similarity 71.2%; Pred. No. 1.1e-100;  
RESULT 421  
ID ADE83448 standard; protein; 345 AA.  
DE Human Protein Q14982, SEQ ID NO 11043.

PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 70.2%; Score 1268; DB 7; Length 345;  
Best Local Similarity 71.2%; Pred. No. 1.1e-100;  
RESULT 422  
ID ADG63207 standard; protein; 345 AA.  
DE Opioid-binding protein/cell adhesion molecule-like protein.  
PN WO2003002765-A2.  
PD 09-JAN-2003.  
PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY LTD.  
Query Match 70.2%; Score 1268; DB 7; Length 345;  
Best Local Similarity 71.2%; Pred. No. 1.1e-100;  
RESULT 423  
ID ADE83446 standard; protein; 345 AA.  
DE Rat Protein P32736, SEQ ID NO 11041.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
Query Match 69.7%; Score 1259; DB 7; Length 345;  
Best Local Similarity 71.2%; Pred. No. 6.6e-100;  
RESULT 424  
ID AAO19641 standard; protein; 335 AA.  
DE Human limbic system associated membrane protein 36-85.  
PN CN1345756-A.  
PD 24-APR-2002.  
PA (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.  
Query Match 51.6%; Score 932.5; DB 5; Length 335;  
Best Local Similarity 53.9%; Pred. No. 9.2e-72;  
RESULT 425  
ID ABJ20235 standard; protein; 338 AA.  
DE Human IG gene related protein SEQ ID NO 58.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 51.6%; Score 931.5; DB 6; Length 338;  
Best Local Similarity 55.4%; Pred. No. 1.1e-71;  
RESULT 426  
ID ADL12675 standard; protein; 338 AA.  
DE Human steroid-induced C3A liver cell protein #60.  
PN US6673549-B1.  
PD 06-JAN-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 51.6%; Score 931.5; DB 8; Length 338;  
Best Local Similarity 55.4%; Pred. No. 1.1e-71;  
RESULT 427  
ID AAW05153 standard; protein; 338 AA.  
DE Rat LAMP residues 1-332.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 51.3%; Score 926.5; DB 2; Length 338;  
Best Local Similarity 55.1%; Pred. No. 3.1e-71;  
RESULT 428  
ID AAW05154 standard; protein; 338 AA.  
DE Rat LAMP residues 1-332.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 51.3%; Score 926.5; DB 2; Length 338;  
Best Local Similarity 55.1%; Pred. No. 3.1e-71;  
RESULT 429  
ID AAW05152 standard; protein; 325 AA.  
DE Human LAMP residues 8-332.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 51.1%; Score 923.5; DB 2; Length 325;  
Best Local Similarity 55.3%; Pred. No. 5.3e-71;  
RESULT 430  
ID AAW05172 standard; protein; 361 AA.

DE Rat LAMP clone 6c.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 50.6%; Score 913; DB 2; Length 361;  
Best Local Similarity 51.7%; Pred. No. 4.9e-70;  
RESULT 431  
ID AAW05157 standard; protein; 308 AA.  
DE Human LAMP residues 8-315.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 50.3%; Score 908; DB 2; Length 308;  
Best Local Similarity 56.3%; Pred. No. 1.1e-69;  
RESULT 432  
ID AAW05158 standard; protein; 315 AA.  
DE Rat LAMP residues 1-315.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 50.2%; Score 907; DB 2; Length 315;  
Best Local Similarity 56.3%; Pred. No. 1.3e-69;  
RESULT 433  
ID AAW05156 standard; protein; 310 AA.  
DE Rat mature LAMP.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 50.1%; Score 905; DB 2; Length 310;  
Best Local Similarity 55.3%; Pred. No. 2e-69;  
RESULT 434  
ID AAW05155 standard; protein; 304 AA.  
DE Human mature LAMP.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 49.9%; Score 902; DB 2; Length 304;  
Best Local Similarity 55.5%; Pred. No. 3.5e-69;  
RESULT 435  
ID ABR39441 standard; protein; 383 AA.  
DE Human GENSET polypeptide clone name SLAMP.  
PN WO2003014151-A2.  
PD 20-FEB-2003.  
PA (GENSET) GENSET SA.  
Query Match 49.4%; Score 893; DB 6; Length 383;  
Best Local Similarity 53.3%; Pred. No. 2.8e-68;  
RESULT 436  
ID AAW05159 standard; protein; 287 AA.  
DE Human LAMP residues 29-315.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 49.1%; Score 886.5; DB 2; Length 287;  
Best Local Similarity 56.6%; Pred. No. 6.9e-68;  
RESULT 437  
ID AAW05160 standard; protein; 287 AA.  
DE Rat LAMP residues 29-315.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 49.0%; Score 885.5; DB 2; Length 287;  
Best Local Similarity 56.6%; Pred. No. 8.5e-68;  
RESULT 438  
ID ADM47275 standard; protein; 203 AA.  
DE Oestrogen regulated protein like NOVX 25b protein.  
PN WO2003083039-A2.  
PD 09-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 48.4%; Score 873.5; DB 7; Length 203;  
Best Local Similarity 54.5%; Pred. No. 5.7e-67;  
RESULT 439  
ID AAG75020 standard; protein; 326 AA.  
DE Human colon cancer antigen protein SEQ ID NO:5784.  
PN WO2001277165-A1.  
PD 05-APR-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 47.2%; Score 852.5; DB 4; Length 326;  
Best Local Similarity 51.6%; Pred. No. 7.1e-65;  
RESULT 440  
ID AAB31212 standard; protein; 354 AA.  
DE Amino acid sequence of human polypeptide PRO6004.  
PN WO200077037-A2.  
PD 21-DEC-2000.  
PA (GETH) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 4; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 441  
ID ABP53580 standard; protein; 354 AA.  
DE Human NOV12a protein SEQ ID NO:24.  
PN WO200262999-A2.  
PD 15-AUG-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 45.6%; Score 823; DB 5; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 442  
ID AA083592 standard; protein; 354 AA.  
DE Human PRO protein, Seq ID No 2.  
PN WO200208288-A2.  
PD 31-JAN-2002.  
PA (GETH) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 5; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 443  
ID ADI28023 standard; protein; 354 AA.  
DE ECMAD protein 7087904CD1.  
PN WO200202634-A2.  
PD 10-JAN-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 45.6%; Score 823; DB 5; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 444  
ID ABU80739 standard; protein; 354 AA.  
DE Human PRO polypeptide #1.  
PN US2003038635-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 6; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 445  
ID ABO25183 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003040014-A1.  
PD 27-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 6; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 446  
ID ABO33705 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003045687-A1.  
PD 06-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 6; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 447  
ID ABU67301 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003032063-A1.  
PD 13-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 6; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 448  
ID ABU72069 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2002177165-A1.



PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 6; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 449  
ID ABU67170 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003032062-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 6; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 450  
ID ABU82048 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003088063-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 6; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 451  
ID ABU79812 standard; protein; 354 AA.  
DE Human secreted/transmembrane protein PRO6004.  
PN US2003032057-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 6; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 452  
ID ABU72228 standard; protein; 354 AA.  
DE Human PRO6004 protein.  
PN US2003050448-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 6; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 453  
ID ADA47302 standard; protein; 354 AA.  
DE Human secreted/transmembrane polypeptide PRO6004.  
PN US2003044844-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 6; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 454  
ID ABU72356 standard; protein; 354 AA.  
DE Human PRO6004 protein.  
PN US2003027988-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 6; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 455  
ID ABO34251 standard; protein; 354 AA.  
DE Human secreted/transmembrane polypeptide PRO 6004.  
PN US2003044934-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 6; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 456  
ID ABO19870 standard; protein; 354 AA.  
DE Human secreted/transmembrane protein PRO6004.  
PN US2003044902-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 7; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 457  
ID ABU72058 standard; protein; 354 AA.  
DE Human membrane bound receptor/protein PRO6004 amino acid sequence.  
PN US2003065147-A1.  
PD 03-APR-2003.

---

PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 7; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 458  
ID ADB83492 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003073814-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 7; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 459  
ID ADB80598 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003088068-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 7; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 460  
ID ADB73139 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003096968-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 7; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 461  
ID ADB78221 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003092889-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 7; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 462  
ID ADB84869 standard; protein; 354 AA.  
DE Human PRO polypeptide #1.  
PN US2003073817-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 7; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 463  
ID ADB77975 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003092886-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 7; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 464  
ID ADB87041 standard; protein; 354 AA.  
DE Human PRO polypeptide #1.  
PN US2003088067-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 7; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 465  
ID ADB84623 standard; protein; 354 AA.  
DE Human PRO polypeptide #1.  
PN US2003092890-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 7; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 466  
ID ADB83738 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003069397-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.



```
RESULT 485
ID ADE20876 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100735-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 486
ID ADE05720 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100728-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 487
ID ADD74949 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100712-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 488
ID ADD73695 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100717-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 489
ID ADD84927 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100722-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 490
ID ADD86753 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100738-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 491
ID ADE20630 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100734-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 492
ID ADE38927 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096362-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 493
ID ADE05474 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100727-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 494
ID ADD85433 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100711-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 495
ID ADD78299 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100737-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 496
ID ADE21122 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100736-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 497
ID ADD77237 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100732-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 498
ID ADE20384 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100733-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 499
ID ADD75449 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100064-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 500
ID ADD73965 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100708-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 501
ID ADD74211 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003100709-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 502
ID ADD75941 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 503
ID ADD85433 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003100718-A1.
PD 29-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
```

DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003100721-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 504  
ID ADE04982 standard; protein; 354 AA.  
DE Human PRO polypeptide #1.  
PN US2003100726-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 505  
ID ADD75195 standard; protein; 354 AA.  
DE Human PRO polypeptide #1.  
PN US2003100714-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 506  
ID ADD76739 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003100715-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 507  
ID ADD86507 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003100719-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 508  
ID ADE41225 standard; protein; 354 AA.  
DE Human secreted/transmembrane polypeptide PRO6004.  
PN US2003104558-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 509  
ID ADD77975 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003100731-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 510  
ID ADD77483 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003100729-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 511  
ID ADD77729 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003100730-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 512  
ID ADD85187 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.

PN US2003100725-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 513  
ID ADD73719 standard; protein; 354 AA.  
DE Human PRO polypeptide #1.  
PN US2003100710-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 514  
ID ADD74457 standard; protein; 354 AA.  
DE Human PRO polypeptide #1.  
PN US2003100713-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 515  
ID ADD76985 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003100716-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 516  
ID ADD85679 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003100720-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 517  
ID ADE05228 standard; protein; 354 AA.  
DE Human PRO polypeptide #1.  
PN US2003100723-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 518  
ID ADD74703 standard; protein; 354 AA.  
DE Human PRO polypeptide #1.  
PN US2003100724-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 519  
ID ADG05515 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003096959-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 520  
ID ADG27069 standard; protein; 354 AA.  
DE Human PRO polypeptide #1.  
PN US2003096962-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.6%; Score 823; DB 8; Length 354;  
Best Local Similarity 47.9%; Pred. No. 2.8e-62;  
RESULT 521  
ID ADG11132 standard; protein; 354 AA.  
DE Novel human secreted and transmembrane protein PRO6004.  
PN US2003096967-A1.

```
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 522
ID ADG11911 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096963-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 523
ID ADP94468 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096964-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 524
ID ADG06564 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096966-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 525
ID ADH38908 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096965-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 526
ID ADG63659 standard; protein; 354 AA.
DE Human secreted/transmembrane polypeptide PRO6004.
PN US2003180796-A1.
PD 25-SEP-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 527
ID ADG33998 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US200406206-A1.
PD 08-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 528
ID ADI33468 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2003096960-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 529
ID ADH69562 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2004019183-A1.
PD 29-JAN-2004.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 530
ID ADI29723 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2003096961-A1.
PD 22-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 531
ID ADM27120 standard; protein; 354 AA.
DE Novel human secreted and transmembrane protein PRO6004.
PN US2004044179-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 532
ID ADK66478 standard; protein; 354 AA.
DE Human PRO polypeptide #1.
PN US2004044180-A1.
PD 04-MAR-2004.
PA (GETH ) GENENTECH INC.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 533
ID ADS82050 standard; protein; 354 AA.
DE Human cancer-associated protein #5.
PN WO2004035789-A1.
PD 29-APR-2004.
PA (GLDS ) LG LIFE SCI LTD.
Query Match 45.6%; Score 823; DB 8; Length 354;
Best Local Similarity 47.9%; Pred. No. 2.8e-62;
RESULT 534
ID ABB98407 standard; protein; 354 AA.
DE Human NOV6, KILON-like protein.
PN WO200255704-A2.
PD 18-JUL-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.5%; Score 822; DB 5; Length 354;
Best Local Similarity 47.9%; Pred. No. 3.4e-62;
RESULT 535
ID ADB64811 standard; protein; 354 AA.
DE Human protein encoded by clone OCBPF20110210.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 45.4%; Score 820; DB 7; Length 354;
Best Local Similarity 47.9%; Pred. No. 5e-62;
RESULT 536
ID ABP53581 standard; protein; 354 AA.
DE Human NOV12b protein SEQ ID NO:26.
PN WO200262999-A2.
PD 15-AUG-2002.
PA (CURA-) CURAGEN CORP.
Query Match 45.3%; Score 819; DB 5; Length 354;
Best Local Similarity 48.6%; Pred. No. 6.1e-62;
RESULT 537
ID ABJ20234 standard; protein; 348 AA.
DE Human IG gene related protein SEQ ID No 57.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 45.1%; Score 815; DB 6; Length 348;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 538
ID ABJ20233 standard; protein; 348 AA.
DE Human IG gene related protein SEQ ID No 56.
PN WO200299040-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 45.1%; Score 815; DB 6; Length 348;
Best Local Similarity 47.5%; Pred. No. 1.3e-61;
RESULT 539
ID AAB44331 standard; protein; 352 AA.
DE Human PRO4993 protein sequence SEQ ID NO:612.
PN WO200053756-A2.
PD 14-SEP-2000.
```

PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 3; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 540  
ID ABO25277 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO4993.  
FN US2003050239-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 6; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 541  
ID ABU72283 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO4993.  
FN US2002192706-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 6; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 542  
ID ABU09489 standard; protein; 352 AA.  
DE Human secreted and transmembrane PRO polypeptide #39.  
FN US2002177553-A1.  
PD 28-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 6; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 543  
ID ABU61161 standard; protein; 352 AA.  
DE Human secreted/transmembrane polypeptide.  
FN US2002169284-A1.  
PD 14-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 6; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 544  
ID ABU80430 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein PRO4993.  
FN US2003004102-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 6; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 545  
ID ADA25150 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO4993.  
FN US2003050241-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 6; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 546  
ID ABO19732 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane protein PRO4993.  
FN US2003050240-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 6; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 547  
ID ADA12812 standard; protein; 352 AA.  
DE Human secreted/transmembrane polypeptide PRO4993.  
FN US2003055216-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 6; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 548  
ID ABO19623 standard; protein; 352 AA.  
DE Novel human secreted and transmembrane polypeptide #91.  
FN US2003049633-A1.  
PD 13-MAR-2003.  
Query Match 45.1%; Score 815; DB 6; Length 352;

Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 549  
ID ADB74118 standard; protein; 352 AA.  
DE Human PRO polypeptide #91.  
FN US2003045462-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 550  
ID ADB76834 standard; protein; 352 AA.  
DE Human PRO polypeptide #91.  
FN US2003083248-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 551  
ID ADC44260 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
FN US2003054986-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 552  
ID ADC62020 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
FN US2003049684-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 553  
ID ADC63984 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
FN US2003054405-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 554  
ID ADC67084 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
FN US2003060406-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 555  
ID ADC69208 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
FN US2003064407-A1.  
PD 03-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 556  
ID ADC63268 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
FN US2003068648-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 557  
ID ADC68333 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
FN US2003069178-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;

RESULT 558  
ID ADE14653 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003072745-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 559  
ID ADE67708 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003073131-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 560  
ID ADE62644 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003073624-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 561  
ID ADE42277 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003104998-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 562  
ID ADE49646 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003096744-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 563  
ID ADE315700 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003203434-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 564  
ID ADE16814 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003203435-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 565  
ID ADD73429 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003203436-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 566  
ID ADD72787 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003194781-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 567  
ID ADE17438 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003203433-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 568  
ID ADF47452 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003195333-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 569  
ID ADG53209 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003216561-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 570  
ID ADG60529 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003206915-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 571  
ID ADI61289 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003077700-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 7; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 572  
ID ADE48946 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003104536-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 8; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 573  
ID ADE90047 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003130181-A1.  
PD 10-JUL-2003.  
PA (ASHK/) ASHKENAZI A J.  
PA (BAKE/) BAKER K P.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GIRM/) GIRMALDI J C.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (KUOS/) KUO S S.  
PA (NAPI/) NAPIER M A.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.

PA (ROYM/) ROY M A.  
PA (SHEL/) SHELTON D L.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 574 47.5%; Pred. No. 1.3e-61;  
ID ADF61687 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003195345-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 575 47.5%; Pred. No. 1.3e-61;  
ID ADF40379 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003198994-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 576 47.5%; Pred. No. 1.3e-61;  
ID ADF46175 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003195148-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 577 47.5%; Pred. No. 1.3e-61;  
ID ADF24571 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003204055-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 578 47.5%; Pred. No. 1.3e-61;  
ID ADF41003 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003199021-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 579 47.5%; Pred. No. 1.3e-61;  
ID ADF23947 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003203402-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 580 47.5%; Pred. No. 1.3e-61;  
ID ADF33930 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003194780-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 581 47.5%; Pred. No. 1.3e-61;  
ID ADF27397 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003199436-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 582 47.5%; Pred. No. 1.3e-61;  
ID ADF28033 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003199437-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 583 47.5%; Pred. No. 1.3e-61;  
ID ADF41627 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003199435-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 584 47.5%; Pred. No. 1.3e-61;  
ID ADF33306 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003211091-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 585 47.5%; Pred. No. 1.3e-61;  
ID ADF25672 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003211092-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 586 47.5%; Pred. No. 1.3e-61;  
ID ADF26773 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003199674-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 587 47.5%; Pred. No. 1.3e-61;  
ID ADF34562 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003194410-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 588 47.5%; Pred. No. 1.3e-61;  
ID ADF46799 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003195344-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 589 47.5%; Pred. No. 1.3e-61;  
ID ADG50785 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003207803-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 590 47.5%; Pred. No. 1.3e-61;  
ID ADG50161 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003215905-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 45.1%; Score 815; DB 8; Length 352;  
RESULT 591 47.5%; Pred. No. 1.3e-61;  
ID ADG52033 standard; protein; 352 AA.



DE Human secreted/transmembrane protein, PRO4993.  
PN US2003215908-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 8; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 592  
ID ADG49537 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003216305-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 8; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 593  
ID ADG48913 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2003216560-A1.  
PD 20-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 8; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 594  
ID ADG51409 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2004005312-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 8; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 595  
ID ADG59353 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2004005657-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 8; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 596  
ID ADG62809 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2004006219-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 8; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 597  
ID ADM17611 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2004048332-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 8; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 598  
ID ADL07445 standard; protein; 352 AA.  
DE Human secreted/transmembrane protein, PRO4993.  
PN US2004063921-A1.  
PD 01-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 45.1%; Score 815; DB 8; Length 352;  
Best Local Similarity 47.5%; Pred. No. 1.3e-61;  
RESULT 599  
ID AAW05167 standard; protein; 252 AA.  
DE Human LAMP residues 46-294.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 44.1%; Score 796.5; DB 2; Length 252;  
Best Local Similarity 56.9%; Pred. No. 3.4e-60;  
RESULT 600  
ID AAW05168 standard; protein; 252 AA.  
DE Rat LAMP residues 46-294.

PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 44.0%; Score 795.5; DB 2; Length 252;  
Best Local Similarity 56.9%; Pred. No. 4.1e-60;  
RESULT 601  
ID ABG96271 standard; protein; 336 AA.  
DE Human immunoglobulin superfamily protein IGSFP-9.  
PN WO200272794-A2.  
PD 19-SEP-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 42.2%; Score 763; DB 5; Length 336;  
Best Local Similarity 50.6%; Pred. No. 3.9e-57;  
RESULT 602  
ID AAE29924 standard; protein; 336 AA.  
DE Human LP289 protein.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 42.2%; Score 763; DB 6; Length 336;  
Best Local Similarity 50.6%; Pred. No. 3.9e-57;  
RESULT 603  
ID ADH71418 standard; protein; 336 AA.  
DE Human protein of the invention NOV11q SEQ ID NO:314.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 42.2%; Score 763; DB 8; Length 336;  
Best Local Similarity 50.6%; Pred. No. 3.9e-57;  
RESULT 604  
ID ADH71412 standard; protein; 336 AA.  
DE Human protein of the invention NOV1n SEQ ID NO:308.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 42.2%; Score 763; DB 8; Length 336;  
Best Local Similarity 50.6%; Pred. No. 3.9e-57;  
RESULT 605  
ID ADH71414 standard; protein; 336 AA.  
DE Human protein of the invention NOV1lo SEQ ID NO:310.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 42.2%; Score 763; DB 8; Length 336;  
Best Local Similarity 50.6%; Pred. No. 3.9e-57;  
RESULT 606  
ID ADH71388 standard; protein; 344 AA.  
DE Human protein of the invention NOV1lb SEQ ID NO:284.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 42.2%; Score 763; DB 8; Length 344;  
Best Local Similarity 50.6%; Pred. No. 4e-57;  
RESULT 607  
ID ADH71390 standard; protein; 325 AA.  
DE Human protein of the invention NOV1lc SEQ ID NO:286.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 42.2%; Score 762; DB 8; Length 325;  
Best Local Similarity 50.5%; Pred. No. 4.5e-57;  
RESULT 608  
ID AAE30252 standard; protein; 306 AA.  
DE Human LP289 mature protein #1.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL ) LILLY & CO ELI.  
Query Match 42.1%; Score 761; DB 6; Length 306;  
Best Local Similarity 52.5%; Pred. No. 5.1e-57;  
RESULT 609  
ID ADH71402 standard; protein; 307 AA.  
DE Human protein of the invention NOV1li SEQ ID NO:298.  
PN WO2003102155-A2.

PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 307;  
Best Local Similarity 52.5%; Pred. No. 5.1e-57;  
RESULT 610  
ID ADH71410 standard; protein; 309 AA.  
DE Human protein of the invention NOV11m SEQ ID NO:306.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 309;  
Best Local Similarity 52.5%; Pred. No. 5.1e-57;  
RESULT 611  
ID ADH71406 standard; protein; 309 AA.  
DE Human protein of the invention NOV11k SEQ ID NO:302.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 309;  
Best Local Similarity 52.5%; Pred. No. 5.1e-57;  
RESULT 612  
ID AE30253 standard; protein; 314 AA.  
DE Human LP289 mature protein #2.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI. 42.1%; Score 761; DB 6; Length 314;  
Best Local Similarity 52.5%; Pred. No. 5.3e-57;  
RESULT 613  
ID ADH71394 standard; protein; 315 AA.  
DE Human protein of the invention NOV11e SEQ ID NO:290.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 315;  
Best Local Similarity 52.5%; Pred. No. 5.3e-57;  
RESULT 614  
ID ABG94637 standard; protein; 319 AA.  
DE Human NOV5b protein.  
PN WO200266643-A2.  
PD 29-AUG-2002.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 5; Length 319;  
Best Local Similarity 52.5%; Pred. No. 5.4e-57;  
RESULT 615  
ID ABG94636 standard; protein; 319 AA.  
DE Human NOV5a protein.  
PN WO200266643-A2.  
PD 29-AUG-2002.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 5; Length 319;  
Best Local Similarity 52.5%; Pred. No. 5.4e-57;  
RESULT 616  
ID ADL35977 standard; protein; 319 AA.  
DE Human NOVX polypeptide #11.  
PN US2003207800-A1.  
PD 06-NOV-2003.  
PA (MALY) MALYANKAR U M. 42.1%; Score 761; DB 8; Length 336;  
Best Local Similarity 50.6%; Pred. No. 7e-57;  
RESULT 623  
ID ADH71386 standard; protein; 336 AA.  
DE Human protein of the invention NOV11a SEQ ID NO:282.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 760; DB 8; Length 336;  
Best Local Similarity 50.6%; Pred. No. 7e-57;  
RESULT 624  
ID ABG94638 standard; protein; 307 AA.  
DE Human NOV5c protein.  
PN WO200266643-A2.  
PD 29-AUG-2002.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 5; Length 307;  
Best Local Similarity 52.5%; Pred. No. 1.1e-56;  
RESULT 617  
ID ADL35979 standard; protein; 319 AA.

DE Human NOVX polypeptide #12.  
PN US2003207800-A1.  
PD 06-NOV-2003.  
PA (MALY) MALYANKAR U M. 42.1%; Score 761; DB 7; Length 319;  
Best Local Similarity 52.5%; Pred. No. 5.4e-57;  
RESULT 618  
ID ADH71400 standard; protein; 319 AA.  
DE Human protein of the invention NOV11h SEQ ID NO:296.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 319;  
Best Local Similarity 52.5%; Pred. No. 5.4e-57;  
RESULT 619  
ID ADH71396 standard; protein; 319 AA.  
DE Human protein of the invention NOV11f SEQ ID NO:292.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 319;  
Best Local Similarity 52.5%; Pred. No. 5.4e-57;  
RESULT 620  
ID ADH71416 standard; protein; 320 AA.  
DE Human protein of the invention NOV11p SEQ ID NO:312.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 320;  
Best Local Similarity 52.5%; Pred. No. 5.4e-57;  
RESULT 621  
ID ADH71398 standard; protein; 325 AA.  
DE Human protein of the invention NOV11g SEQ ID NO:294.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 8; Length 325;  
Best Local Similarity 52.5%; Pred. No. 5.5e-57;  
RESULT 622  
ID ADH71422 standard; protein; 336 AA.  
DE Human protein of the invention NOV11s SEQ ID NO:318.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 760; DB 8; Length 336;  
Best Local Similarity 50.6%; Pred. No. 7e-57;  
RESULT 623  
ID ADH71386 standard; protein; 336 AA.  
DE Human protein of the invention NOV11a SEQ ID NO:282.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 760; DB 8; Length 336;  
Best Local Similarity 50.6%; Pred. No. 7e-57;  
RESULT 624  
ID ABG94638 standard; protein; 307 AA.  
DE Human NOV5c protein.  
PN WO200266643-A2.  
PD 29-AUG-2002.  
PA (CURA-) CURAGEN CORP. 42.1%; Score 761; DB 5; Length 307;  
Best Local Similarity 52.5%; Pred. No. 1.1e-56;  
RESULT 617  
ID ADL35979 standard; protein; 319 AA.

DE Novel human secreted or membrane-associated protein #25.

Query Match 37.7%; Score 681.5; DB 5; Length 351;  
Best Local Similarity 50.7%; Pred. No. 4.4e-50;  
RESULT 640  
ID ABG13848 standard; protein; 141 AA.  
DE Novel human diagnostic protein #13839.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 33.4%; Score 603; DB 4; Length 141;  
Best Local Similarity 86.6%; Pred. No. 7.5e-44;  
RESULT 641  
ID AAE30271 standard; protein; 294 AA.  
DE Human LP319b protein variant #2.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 33.4%; Score 603; DB 6; Length 294;  
Best Local Similarity 45.0%; Pred. No. 2e-43;  
RESULT 642  
ID AAE30270 standard; protein; 286 AA.  
DE Human LP319b protein variant #1.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 33.2%; Score 600; DB 6; Length 286;  
Best Local Similarity 45.0%; Pred. No. 3.6e-43;  
RESULT 643  
ID ADP29917 standard; protein; 222 AA.  
DE Human secreted protein SEQ ID #694.  
PN WO200403732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 33.2%; Score 599.5; DB 8; Length 222;  
Best Local Similarity 54.0%; Pred. No. 2.8e-43;  
RESULT 644  
ID ABG13847 standard; protein; 130 AA.  
DE Novel human diagnostic protein #13838.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 31.5%; Score 569.5; DB 4; Length 130;  
Best Local Similarity 88.9%; Pred. No. 5.2e-41;  
RESULT 645  
ID AAE30269 standard; protein; 234 AA.  
DE Human LP319b protein mature sequence #2.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 29.2%; Score 527; DB 6; Length 234;  
Best Local Similarity 53.2%; Pred. No. 5.4e-37;  
RESULT 646  
ID AAE29927 standard; protein; 256 AA.  
DE Human LP319b protein.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 29.2%; Score 527; DB 6; Length 256;  
Best Local Similarity 53.2%; Pred. No. 6.1e-37;  
RESULT 647  
ID ABG13816 standard; protein; 872 AA.  
DE Novel human diagnostic protein #13807.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 29.1%; Score 525.5; DB 4; Length 872;  
Best Local Similarity 43.4%; Pred. No. 4.4e-36;  
RESULT 648  
ID ADE08994 standard; protein; 872 AA.  
DE Novel protein-related contig polypeptide sequence #60.  
PN WO2003054152-A2.  
PD 03-JUL-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 29.1%; Score 525.5; DB 7; Length 872;

Best Local Similarity 43.4%; Pred. No. 4.4e-36;  
RESULT 649  
ID AAE30268 standard; protein; 226 AA.  
DE Human LP319b protein mature sequence #1.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 28.0%; Score 505; DB 6; Length 226;  
Best Local Similarity 53.0%; Pred. No. 4e-35;  
RESULT 650  
ID AAE30264 standard; protein; 211 AA.  
DE Human LP319a protein mature sequence #1.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 26.1%; Score 472; DB 6; Length 211;  
Best Local Similarity 54.1%; Pred. No. 2.6e-32;  
RESULT 651  
ID AAE30265 standard; protein; 222 AA.  
DE Human LP319a protein mature sequence #2.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 26.1%; Score 472; DB 6; Length 222;  
Best Local Similarity 54.1%; Pred. No. 2.8e-32;  
RESULT 652  
ID AAE29926 standard; protein; 241 AA.  
DE Human LP319a protein.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 26.1%; Score 472; DB 6; Length 241;  
Best Local Similarity 54.1%; Pred. No. 3.1e-32;  
RESULT 653  
ID ABB69485 standard; protein; 413 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 35247.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 18.7%; Score 338.5; DB 4; Length 413;  
Best Local Similarity 28.0%; Pred. No. 2.1e-20;  
RESULT 654  
ID ABB65642 standard; protein; 315 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 23718.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 18.4%; Score 333; DB 4; Length 315;  
Best Local Similarity 31.9%; Pred. No. 4.4e-20;  
RESULT 655  
ID ABB62574 standard; protein; 545 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 14514.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 16.9%; Score 306; DB 4; Length 545;  
Best Local Similarity 28.9%; Pred. No. 2e-17;  
RESULT 656  
ID ABB58947 standard; protein; 333 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 3633.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 16.5%; Score 297.5; DB 4; Length 333;  
Best Local Similarity 29.7%; Pred. No. 5.4e-17;  
RESULT 657  
ID ADS10483 standard; protein; 2537 AA.  
DE Human therapeutic protein - SEQ ID 720.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 16.1%; Score 290.5; DB 8; Length 2537;  
Best Local Similarity 29.8%; Pred. No. 3.5e-15;

```

RESULT 658
ID ABU12083 standard; protein; 2572 AA.
DE Human NOV25b CG93858-02 protein SEQ ID 86.
PN WO200281625-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 290.5; DB 6; Length 2572;
Best Local Similarity 29.8%; Pred. No. 3.6e-15;
RESULT 659
ID ADK60225 standard; protein; 2673 AA.
DE Angiogenesis differentially expressed protein GS-P52.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 2673;
Best Local Similarity 29.8%; Pred. No. 3.8e-15;
RESULT 660
ID ADK60526 standard; protein; 2673 AA.
DE Angiogenesis differentially expressed protein GS-P52.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 2673;
Best Local Similarity 29.8%; Pred. No. 3.8e-15;
RESULT 661
ID ADP73149 standard; protein; 2673 AA.
DE Angiogenesis inhibitor human protein sequence, GS-P52.
PN FR2843753-A1.
PD 27-FEB-2004.
PA (GENE/) GENE S.
PA (ALMS/) AL M S.
Query Match 16.1%; Score 290.5; DB 8; Length 2673;
Best Local Similarity 29.8%; Pred. No. 3.8e-15;
RESULT 662
ID ABU69135 standard; protein; 4495 AA.
DE Human NOVX polypeptide #10.
PN WO200290504-A2.
PD 14-NOV-2002.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 290.5; DB 6; Length 4495;
Best Local Similarity 29.8%; Pred. No. 7.7e-15;
RESULT 663
ID ADH72106 standard; protein; 4495 AA.
DE Human protein of the invention NOV43c SEQ ID NO:1002.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 16.1%; Score 290.5; DB 8; Length 4495;
Best Local Similarity 29.8%; Pred. No. 7.7e-15;
RESULT 664
ID AD008273 standard; protein; 4495 AA.
DE Human NOVX polypeptide #10.
PN US2004018594-A1.
PD 29-JAN-2004.
PA (ALSO/) ALSOBROOK J P.
PA (ANDE/) ANDERSON D W.
PA (BOLD/) BOLDOG F L.
PA (BURG/) BURGESS C E.
PA (CASM/) CASMAN S J.
PA (CHAP/) CHAPOVAL A.
PA (EDIN/) EDINGER S R.
PA (GERL/) GERLACH V.
PA (GORM/) GORMAN L.
PA (GUNT/) GUNTHER E.
PA (GUOX/) GUO X S.
PA (KEKU/) KEKUDA R.
PA (LEPL/) LEPLEY D M.
PA (LIUL/) LI L.
PA (LIUX/) LIU X.
PA (MALY/) MALYANKAR U M.
PA (MILL/) MILLER C E.
PA (MILL/) MILLET I.
PA (PADI/) PADIGARU M.
PA (PATT/) PATTURAJAN M.
PA (PENA/) PENNA C E A.
PA (RIEG/) RIEGER D K.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (SPYT/) SPYTEK K A.
PA (TAUP/) TAUPIER R J.
PA (VERN/) VERNET C A M.
PA (VOSS/) VOSS E Z.
PA (ZERH/) ZERHUSEN B D.
Query Match 16.1%; Score 290.5; DB 8; Length 4495;
Best Local Similarity 29.8%; Pred. No. 7.7e-15;
RESULT 665
ID ADJ70089 standard; protein; 5636 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1895.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 16.1%; Score 290.5; DB 7; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1e-14;
RESULT 666
ID ADJ83137 standard; protein; 5636 AA.
DE Human hemicentin protein - SEQ ID 128.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATT/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 16.1%; Score 290.5; DB 7; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1e-14;
RESULT 667
ID ADK60205 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836687-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1e-14;
RESULT 668
ID ADK60506 standard; protein; 5636 AA.
DE Angiogenesis differentially expressed protein GS-P29.
PN FR2836686-A1.
PD 05-SEP-2003.
PA (GENE-) GENE SIGNAL.
PA (ALMA/) AL MAHMOOD S.
Query Match 16.1%; Score 290.5; DB 8; Length 5636;
Best Local Similarity 31.1%; Pred. No. 1e-14;

```

Best Local Similarity 31.1%; Pred. No. 1e-14;  
RESULT 669  
ID ADP73129 standard; protein; 5636 AA.  
DE Angiogenesis inhibitor human protein sequence, GS-P29.  
FN FR2843753-A1.  
PD 27-FEB-2004.  
PA (GENE/) GENE S.  
PA (ALMS/) AL M S.  
Query Match 16.1%; Score 290.5; DB 8; Length 5636;  
Best Local Similarity 31.1%; Pred. No. 1e-14;  
RESULT 670  
ID ADG39844 standard; protein; 1708 AA.  
DE Protein similar to human NOV9 #5.  
FN US2003203843-A1.  
PD 30-OCT-2003.  
PA (PENA/) PENA C E A.  
PA (GUOX/) GUO X.  
PA (SHIM/) SHIMKETS R A.  
PA (PADI/) PADIGARU M.  
PA (KEKU/) KEKUDA R.  
PA (SPYT/) SPYTEK K A.  
PA (MEHR/) MEHRABAN F.  
PA (TOPP/) TOPPER J N.  
PA (WASS/) WASSERMAN U M.  
PA (MALLY/) MALLYANKAR U M.  
PA (EDIN/) EDINGER S R.  
PA (SMIT/) SMITHSON G.  
PA (GUNT/) GUNTHER E.  
PA (KOMU/) KOMUVES L.  
Query Match 16.0%; Score 289.5; DB 7; Length 1708;  
Best Local Similarity 29.8%; Pred. No. 2.5e-15;  
RESULT 671  
ID ADG39840 standard; protein; 1708 AA.  
DE Protein similar to human NOV9 #1.  
FN US2003203843-A1.  
PD 30-OCT-2003.  
PA (PENA/) PENA C E A.  
PA (GUOX/) GUO X.  
PA (SHIM/) SHIMKETS R A.  
PA (PADI/) PADIGARU M.  
PA (KEKU/) KEKUDA R.  
PA (SPYT/) SPYTEK K A.  
PA (MEHR/) MEHRABAN F.  
PA (TOPP/) TOPPER J N.  
PA (WASS/) WASSERMAN U M.  
PA (EDIN/) EDINGER S R.  
PA (SMIT/) SMITHSON G.  
PA (GUNT/) GUNTHER E.  
PA (KOMU/) KOMUVES L.  
Query Match 16.0%; Score 288.5; DB 8; Length 707;  
Best Local Similarity 31.1%; Pred. No. 9.1e-16;  
RESULT 672  
ID ABU69134 standard; protein; 707 AA.  
DE Human NOVX polypeptide #9.  
FN WO200290504-A2.  
PD 14-NOV-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 16.0%; Score 288.5; DB 6; Length 707;  
Best Local Similarity 31.1%; Pred. No. 9.1e-16;  
RESULT 673  
ID ADH72102 standard; protein; 707 AA.  
DE Human protein of the invention NOV43a SEQ ID NO:998.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 16.0%; Score 288.5; DB 8; Length 707;  
Best Local Similarity 31.1%; Pred. No. 9.1e-16;  
RESULT 674  
ID ADO08271 standard; protein; 707 AA.  
DE Human NOVX polypeptide #9.  
FN US2004018594-A1.  
PD 29-JAN-2004.

(ALSO/) ALSOBROOK J P.  
(ANDE/) ANDERSON D W.  
(BOLD/) BOLDOG F L.  
(BURG/) BURGESS C E.  
(CASM/) CASMAN S J.  
(CHAP/) CHAPOVAL A.  
(EDIN/) EDINGER S R.  
(GERL/) GERLACH V.  
(GORM/) GORMAN L.  
(GUNT/) GUNTHER E.  
(GUOX/) GUO X S.  
(KEKU/) KEKUDA R.  
(LEPL/) LEPLEY D M.  
(LILL/) LI L.  
(LIUX/) LIU X.  
(MALLY/) MALLYANKAR U M.  
(MILL/) MILLER C E.  
(MILL/) MILLET I.  
(PADI/) PADIGARU M.  
(PATT/) PATTURAJAN M.  
(PENA/) PENA C E A.  
(RIEG/) RIEGER D K.  
(SHEN/) SHENOY S G.  
(SHIM/) SHIMKETS R A.  
(SPYT/) SPYTEK K A.  
(TAUP/) TAUPIER R J.  
(VERN/) VERNET C A M.  
(VOSS/) VOSS E Z.  
(ZERH/) ZERHUSEN B D.  
Query Match 16.0%; Score 288.5; DB 8; Length 707;  
Best Local Similarity 31.1%; Pred. No. 9.1e-16;  
RESULT 675  
ID ADH72104 standard; protein; 712 AA.  
DE Human protein of the invention NOV43b SEQ ID NO:1000.  
FN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 16.0%; Score 288.5; DB 8; Length 712;  
Best Local Similarity 31.1%; Pred. No. 9.2e-16;  
RESULT 676  
ID ABU99129 standard; protein; 961 AA.  
DE Novel human GPCR related protein NOV9b.  
FN WO200299116-A2.  
PD 12-DEC-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 16.0%; Score 288.5; DB 6; Length 961;  
Best Local Similarity 30.5%; Pred. No. 1.4e-15;  
RESULT 677  
ID ADM93823 standard; protein; 961 AA.  
DE Human NOV protein #21.  
FN US2004009480-A1.  
PD 15-JAN-2004.  
PA (ANDE/) ANDERSON D W.  
PA (BAUM/) BAUMGARTNER J C.  
PA (BOLD/) BOLDOG F L.  
PA (CASM/) CASMAN S J.  
PA (EDIN/) EDINGER S R.  
PA (GANG/) GANGOLLI E A.  
PA (GERL/) GERLACH V.  
PA (GORM/) GORMAN L.  
PA (GUOX/) GUO X S.  
PA (HJAL/) HJALT T.  
PA (KEKU/) KEKUDA R.  
PA (LILL/) LI L.  
PA (MACD/) MACDOUGALL J R.  
PA (MALLY/) MALLYANKAR U M.  
PA (MILL/) MILLET I.  
PA (PADI/) PADIGARU M.  
PA (PATT/) PATTURAJAN M.  
PA (PENA/) PENA C E A.  
PA (RAST/) RASTELLI L.  
PA (SHIM/) SHIMKETS R A.  
PA (STON/) STONE D J.

PA (SPYT/) SPYTEK K A.  
PA (VERN/) VERNET C A M.  
PA (VOSS/) VOSS E Z.  
PA (ZERH/) ZERHUSEN B D.  
Query Match 16.0%; Score 288.5; DB 8; Length 961;  
Best Local Similarity 30.5%; Pred. No. 1.4e-15;  
RESULT 678  
ID ABG03933 standard; protein; 1240 AA.  
DE Novel human diagnostic protein #3924.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 16.0%; Score 288.5; DB 4; Length 1240;  
Best Local Similarity 31.1%; Pred. No. 2e-15;  
RESULT 679  
ID AAB47771 standard; protein; 1336 AA.  
DE Human thrombospondin protein, BTL 012.  
PN WO200174852-A2.  
PD 11-OCT-2001.  
PA (FARB ) BAYER CORP.  
Query Match 16.0%; Score 288.5; DB 5; Length 1336;  
Best Local Similarity 31.1%; Pred. No. 2.2e-15;  
RESULT 680  
ID ABU12084 standard; protein; 1902 AA.  
DE Human NOV25c CG56914-03 protein SEQ ID 88.  
PN WO200281625-A2.  
PD 17-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 16.0%; Score 288.5; DB 6; Length 1902;  
Best Local Similarity 31.1%; Pred. No. 3.5e-15;  
RESULT 681  
ID ADH72108 standard; protein; 1902 AA.  
DE Human protein of the invention NOV43d SEQ ID NO:1004.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 16.0%; Score 288.5; DB 8; Length 1902;  
Best Local Similarity 31.1%; Pred. No. 3.5e-15;  
RESULT 682  
ID ADI16058 standard; protein; 1953 AA.  
DE G-coupled protein receptor related polypeptide, SEQ ID No 88.  
PN WO200283841-A2.  
PD 24-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 16.0%; Score 288.5; DB 7; Length 1953;  
Best Local Similarity 31.1%; Pred. No. 3.6e-15;  
RESULT 683  
ID ADJ93997 standard; protein; 1953 AA.  
DE Human G-coupled protein receptor-related protein #44.  
PN US2004006205-A1.  
PD 08-JAN-2004.  
PA (LILL/) LI L.  
PA (GERL/) GERLACH V.  
PA (LIUX/) LIU X.  
PA (MILL/) MILLER C E.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PENA/) PENNA C E A.  
PA (SHEN/) SHENOY S G.  
PA (ZHON/) ZHONG H.  
PA (SMIT/) SMITHSON G.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (VOSS/) VOSS E Z.  
PA (VERN/) VERNET C A.  
PA (MACD/) MACDOUGALL J R.  
PA (RAST/) RASTELLI L.  
PA (ANDE/) ANDERSON D W.  
PA (ZHON/) ZHONG M.  
PA (MEZE/) MEZES P S.  
PA (FURT/) FURTAK K.  
PA (PATT/) PATTURAJAN M.  
PA (BURG/) BURGESS C E.

PA (MALY/) MALYANKAR U M.  
PA (SHIM/) SHINKETS R A.  
PA (TAUP/) TAUPIER R J.  
PA (EDIN/) EDINGER S.  
PA (MAZU/) MAZUR A.  
Query Match 16.0%; Score 288.5; DB 8; Length 1953;  
Best Local Similarity 31.1%; Pred. No. 3.6e-15;  
RESULT 684  
ID ADJ83136 standard; protein; 3645 AA.  
DE Human hemocentrin protein - SEQ ID 127.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (LEPL/) LEPPLEY D M.  
PA (BURG/) BURGESS C E.  
PA (SHIM/) SHINKETS R A.  
PA (GROS/) GROSSE W M.  
PA (SZEK/) SZEXERES E S.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (GORM/) GORMAN L.  
PA (GANG/) GANGOLLI E A.  
PA (FERN/) FERNANDES E R.  
PA (RIEG/) RIEGER D K.  
PA (EDIN/) EDINGER S R.  
PA (GUNT/) GUNTHER E.  
PA (MILL/) MILLET I.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MACD/) MACDOUGALL J R.  
PA (SMIT/) SMITHSON G.  
Query Match 16.0%; Score 288.5; DB 7; Length 3645;  
Best Local Similarity 31.1%; Pred. No. 8.6e-15;  
RESULT 685  
ID ASP60991 standard; protein; 5635 AA.  
DE Novel human protein. SEQ ID 78.  
PN WO200250105-A1.  
PD 27-JUN-2002.  
PA (SMIK ) SMITHKLINE BEECHAM CORP.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (GLAX ) GLAXO GROUP LTD.  
Query Match 16.0%; Score 288.5; DB 5; Length 5635;  
Best Local Similarity 31.1%; Pred. No. 1.6e-14;  
RESULT 686  
ID ADG39841 standard; protein; 1708 AA.  
DE Protein similar to human NOV9 #2.  
PN US2003203843-A1.  
PD 30-OCT-2003.  
PA (PENA/) PENNA C E A.  
PA (GUOX/) GUO X.  
PA (SHIM/) SHINKETS R A.  
PA (PADI/) PADIGARU M.  
PA (KEKU/) KEKUDA R.  
PA (SPYT/) SPYTEK K A.  
PA (MEHR/) MEHRABAN F.  
PA (TOPP/) TOPPER J N.  
PA (MALY/) MALYANKAR U M.  
PA (WASS/) WASSERMAN S M.  
PA (EDIN/) EDINGER S R.  
PA (SMIT/) SMITHSON G.  
PA (GUNT/) GUNTHER E.  
PA (KOMU/) KOMUVES L.  
Query Match 15.9%; Score 287.5; DB 7; Length 1708;  
Best Local Similarity 31.1%; Pred. No. 3.7e-15;  
RESULT 687  
ID ABB63044 standard; protein; 467 AA.

DE Drosophila melanogaster polypeptide SEQ ID NO 15924.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 15.8%; Score 284.5; DB 4; Length 467;  
Best Local Similarity 26.1%; Pred. No. 1.1e-15;  
RESULT 688  
ID ADE63330 standard; protein; 858 AA.  
DE Rat Protein P13596, SEQ ID NO 9268.  
PN WO2001016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 15.4%; Score 277.5; DB 7; Length 858;  
Best Local Similarity 25.5%; Pred. No. 1.1e-14;  
RESULT 689  
ID ADA55624 standard; protein; 733 AA.  
DE Human protein, SEQ ID 3192.  
PN EPI293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 15.3%; Score 276; DB 6; Length 733;  
Best Local Similarity 25.7%; Pred. No. 1.1e-14;  
RESULT 690  
ID ADE63332 standard; protein; 761 AA.  
DE Human Protein P13592, SEQ ID NO 9270.  
PN WO2001016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 15.3%; Score 276; DB 7; Length 761;  
Best Local Similarity 25.7%; Pred. No. 1.2e-14;  
RESULT 691  
ID AA188565 standard; protein; 848 AA.  
DE Human NCAM 140kd isoform precursor amino acid sequence.  
PN WO200118801-A2.  
PD 06-APR-2000.  
PA (RONN/) RONN L C B.  
PA (BOCK/) BOCK E.  
PA (HOLM/) HOLM A.  
PA (OLSE/) OLSEN M.  
PA (OLSE/) OLSEN M.  
PA (OSTE/) OSTERGAARD S.  
PA (JENS/) JENSEN P H.  
PA (POUL/) POULSEN F M.  
PA (SORO/) SOROKA V.  
PA (RALE/) RALETS I.  
PA (BERE/) BEREZIN V.  
Query Match 15.3%; Score 276; DB 3; Length 848;  
Best Local Similarity 25.7%; Pred. No. 1.4e-14;  
RESULT 692  
ID AAE17222 standard; protein; 848 AA.  
DE Human 140kd NCAM isoform protein.  
PN WO200196364-A2.  
PD 20-DEC-2001.  
PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.  
PA (UNLO) KINGS COLLEGE LONDON.  
Query Match 15.3%; Score 276; DB 5; Length 848;  
Best Local Similarity 25.7%; Pred. No. 1.4e-14;  
RESULT 693  
ID AD124546 standard; protein; 848 AA.  
DE Human modifier of Chk1 (MCHK) protein SEQ ID NO:96.  
PN WO2004004785-A1.  
PD 15-JAN-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match 15.3%; Score 276; DB 8; Length 848;  
Best Local Similarity 25.7%; Pred. No. 1.4e-14;  
RESULT 694  
ID ADE28603 standard; protein; 853 AA.  
DE Bovine NCAM-140 protein - SED ID 513.  
PN WO2003048326-A2.  
PD 12-JUN-2003.  
PA (HYSE-) HYSEQ INC.

Query Match 15.3%; Score 275.5; DB 7; Length 853;  
Best Local Similarity 25.5%; Pred. No. 1.6e-14;  
RESULT 695  
ID ADJ36019 standard; protein; 90 AA.  
DE Human NOVX-related polypeptide #17.  
PN US2003207800-A1.  
PD 06-NOV-2003.  
PA (MALY/) MALYANKAR U M.  
PA (SHEN/) SHENOY S G.  
PA (SEY/) SEYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (GUOX/) GUO X.  
PA (KEKU/) KEKUDA R.  
PA (GANG/) GANGOLLI E A.  
PA (SHIM/) SHIMKETS R A.  
PA (TAUP/) TAUPIER R J.  
PA (LILL/) LI L.  
PA (PADI/) PADIGARU M.  
Query Match 15.2%; Score 275; DB 7; Length 90;  
Best Local Similarity 61.8%; Pred. No. 7.9e-16;  
RESULT 696  
ID ADD25619 standard; protein; 848 AA.  
DE Binding domain-immunoglobulin fusion protein-associated protein #87.  
PN US2003118592-A1.  
PD 26-JUN-2003.  
PA (GENE-) GENE-CRAFT INC.  
Query Match 15.2%; Score 275; DB 7; Length 848;  
Best Local Similarity 25.7%; Pred. No. 1.7e-14;  
RESULT 697  
ID AAE37177 standard; protein; 1477 AA.  
DE Human LRRCAPS protein #2.  
PN WO2003035831-A2.  
PD 01-MAY-2003.  
PA (EXEL-) EXELIXIS INC.  
Query Match 15.2%; Score 274; DB 6; Length 1477;  
Best Local Similarity 29.2%; Pred. No. 4.4e-14;  
RESULT 698  
ID ADH48824 standard; protein; 1356 AA.  
DE NOV45B protein sequence, SEQ ID 108.  
PN WO200268652-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.1%; Score 273.5; DB 5; Length 1356;  
Best Local Similarity 29.6%; Pred. No. 4.4e-14;  
RESULT 699  
ID ADH48822 standard; protein; 1426 AA.  
DE NOV45A protein sequence, SEQ ID 106.  
PN WO200268652-A2.  
PD 06-SEP-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 15.0%; Score 271.5; DB 5; Length 1426;  
Best Local Similarity 29.6%; Pred. No. 6.9e-14;  
RESULT 700  
ID AAO30845 standard; protein; 859 AA.  
DE Human cell adhesion and extracellular matrix protein (CADECM)-35.  
PN WO2003047526-A2.  
PD 12-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 15.0%; Score 271; DB 7; Length 859;  
Best Local Similarity 24.8%; Pred. No. 3.8e-14;  
RESULT 701  
ID ABB68566 standard; protein; 729 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 32490.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 15.0%; Score 270; DB 4; Length 729;  
Best Local Similarity 26.7%; Pred. No. 3.7e-14;  
RESULT 702  
ID AAU18023 standard; protein; 152 AA.  
DE Human immunoglobulin polypeptide SEQ ID NO 168.  
PN WO200155315-A2.



PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 14.9%; Score 269; DB 4; Length 152;  
Best Local Similarity 42.3%; Pred. No. 5.3e-15;  
RESULT 703  
ID ADB31647 standard; protein; 152 AA.  
DE Human novel protein SEQ ID NO 168.  
FN US2003077606-A1.  
PD 24-APR-2003.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 14.9%; Score 269; DB 7; Length 152;  
Best Local Similarity 42.3%; Pred. No. 5.3e-15;  
RESULT 704  
ID ADR66889 standard; protein; 1469 AA.  
DE Human prostatic carcinoma derived DNA SEQ ID 187 #4.  
FN WO2004076614-A2.  
PA (HINZ-) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 14.9%; Score 268.5; DB 8; Length 1469;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 705  
ID ADR65991 standard; protein; 1469 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 187 #1.  
FN WO2004076614-A2.  
PA (HINZ-) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 14.9%; Score 268.5; DB 8; Length 1469;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 706  
ID ADJ35717 standard; protein; 1479 AA.  
DE Human peroxidasin-melanoma antigen-related protein.  
FN WO2004019893-A2.  
PD 11-MAR-2004.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match 14.9%; Score 268.5; DB 8; Length 1479;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 707  
ID AAW81030 standard; protein; 1496 AA.  
DE Melanoma associated antigen MG50.  
FN WO9855133-A1.  
PD 10-DEC-1998.  
PA (REGC-) UNIV CALIFORNIA.  
PA (UYSC-) UNIV SOUTHERN CALIFORNIA.  
Query Match 14.9%; Score 268.5; DB 2; Length 1496;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 708  
ID AAV70469 standard; protein; 1496 AA.  
DE Human p53 target molecule, PRG2 protein.  
FN WO200012526-A1.  
PD 09-MAR-2000.  
PA (UYPR-) UNIV PRINCETON.  
Query Match 14.9%; Score 268.5; DB 3; Length 1496;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 709  
ID ABU03498 standard; protein; 1496 AA.  
DE Angiogenesis-associated human protein sequence #43.  
FN WO200279492-A2.  
PD 10-OCT-2002.  
PA (EOSB-) EOS BIOTECHNOLOGY INC.  
Query Match 14.9%; Score 268.5; DB 6; Length 1496;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 710  
ID ADD89024 standard; protein; 1496 AA.  
DE TAT264.  
FN WO2003057160-A2.

PD 17-JUL-2003.  
PA (GETH-) GENENTECH INC.  
Query Match 14.9%; Score 268.5; DB 7; Length 1496;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 711  
ID ADF28706 standard; protein; 1496 AA.  
DE Human peroxidasin-like MG50 protein - SED ID 616.  
FN WO2003048326-A2.  
PD 12-JUN-2003.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.9%; Score 268.5; DB 7; Length 1496;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 712  
ID ADQ18902 standard; protein; 1496 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 1721.  
FN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 14.9%; Score 268.5; DB 8; Length 1496;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 713  
ID ADQ89920 standard; protein; 1496 AA.  
DE Antagonist of cell cycle progression polypeptide #175.  
FN WO2004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
Query Match 14.9%; Score 268.5; DB 8; Length 1496;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 714  
ID ADO89914 standard; protein; 1496 AA.  
DE Antagonist of cell cycle progression polypeptide #172.  
FN WO2004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
Query Match 14.9%; Score 268.5; DB 8; Length 1496;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 715  
ID ADR66092 standard; protein; 1496 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 288 #1.  
FN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ-) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 14.9%; Score 268.5; DB 8; Length 1496;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 716  
ID ADR66434 standard; protein; 1496 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 288 #2.  
FN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ-) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 14.9%; Score 268.5; DB 8; Length 1496;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 717  
ID ADR66434 standard; protein; 1496 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 288 #2.  
FN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ-) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (ROSE/) ROSENTHAL A.  
PA (HERM/) HERMANN K.  
PA (PILA/) PILARSKY C.  
Query Match 14.9%; Score 268.5; DB 8; Length 1496;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 718  
ID ABB11587 standard; peptide; 1498 AA.  
DE Human peroxidasin homologue, SEQ ID NO:1957.  
FN WO200157188-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.9%; Score 268.5; DB 4; Length 1498;  
Best Local Similarity 28.8%; Pred. No. 1.3e-13;  
RESULT 719  
ID ABO00762 standard; protein; 1498 AA.  
DE Polypeptide encoded by novel human contig #13.  
FN WO2003023013-A2.  
PD 20-MAR-2003.

PA (HYSE-) HYSEQ INC. 14.9%; Score 268.5; DB 6; Length 1498;  
Query Match 28.8%; Pred. No. 1.3e-13;  
RESULT 719  
ID AAG02771 standard; protein; 58 AA.  
DE Human secreted protein, SEQ ID NO: 6852.  
PN EPI033401-A2.  
PD 06-SEP-2000.  
PA (GEST-) GENSET.  
Query Match 14.8%; Score 267; DB 3; Length 58;  
Best Local Similarity 86.2%; Pred. No. 2.1e-15;  
RESULT 720  
ID ABB97902 standard; protein; 142 AA.  
DE Human secretory polypeptide (SPTM) 154.  
PN W0200220756-A2.  
PD 14-MAR-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 14.6%; Score 263; DB 5; Length 142;  
Best Local Similarity 44.1%; Pred. No. 1.6e-14;  
RESULT 721  
ID AAY13563 standard; protein; 1395 AA.  
DE Drosophila Robo 1 polypeptide.  
PN W09925833-A1.  
PD 27-MAY-1999.  
PA (REGC-) UNIV CALIFORNIA.  
Query Match 14.5%; Score 261; DB 2; Length 1395;  
Best Local Similarity 26.1%; Pred. No. 5.4e-13;  
RESULT 722  
ID AAY08401 standard; protein; 1395 AA.  
DE Drosophila sp. ROBO1 protein.  
PN W09920764-A1.  
PD 29-APR-1999.  
PA (REGC-) UNIV CALIFORNIA.  
Query Match 14.5%; Score 261; DB 2; Length 1395;  
Best Local Similarity 26.1%; Pred. No. 5.4e-13;  
RESULT 723  
ID ABB62052 standard; protein; 496 AA.  
DE Fruitfly nerve cell growth modulator SLIT-1-associated sequence #1.  
PN US2003170727-A1.  
PD 11-SEP-2003.  
PA (GOOD/) GOODMAN C S.  
PA (KIDD/) KIDD T.  
PA (BROS/) BROSE K.  
PA (TESS/) TESSIER-LAVIGNE M.  
Query Match 14.5%; Score 261; DB 7; Length 1395;  
Best Local Similarity 26.1%; Pred. No. 5.4e-13;  
RESULT 724  
ID ABB62052 standard; protein; 496 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 12948.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 14.4%; Score 260.5; DB 4; Length 496;  
Best Local Similarity 26.2%; Pred. No. 1.5e-13;  
RESULT 725  
ID ABB68257 standard; protein; 1395 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 31563.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 14.4%; Score 260; DB 4; Length 1395;  
Best Local Similarity 26.1%; Pred. No. 6.6e-13;  
RESULT 726  
ID AAY53666 standard; protein; 4412 AA.  
DE Sequence gi/1017427/emb/CAA62189 from an alignment with protein 608.  
PN W09960164-A1.  
PD 25-NOV-1999.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 14.3%; Score 259; DB 3; Length 4412;  
Best Local Similarity 29.6%; Pred. No. 3.9e-12;  
RESULT 727  
ID ABB74786 standard; protein; 31267 AA.  
DE Human RGS11 protein.

PN W02002103355-A1.  
PD 27-DEC-2002.  
PA (TAKE-) TAKEDA CHEM IND LTD.  
Query Match 14.3%; Score 259; DB 6; Length 31267;  
Best Local Similarity 29.6%; Pred. No. 5.7e-11;  
RESULT 728  
ID ADQ89964 standard; protein; 34350 AA.  
DE Antagonist of cell cycle progression polypeptide #197.  
PN W02004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
Query Match 14.3%; Score 259; DB 8; Length 34350;  
Best Local Similarity 29.6%; Pred. No. 6.4e-11;  
RESULT 729  
ID ADM74171 standard; protein; 381 AA.  
DE Human NOV3A protein sequence SeqID10.  
PN W02004015079-A2.  
PD 19-FEB-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 14.3%; Score 258.5; DB 8; Length 381;  
Best Local Similarity 27.4%; Pred. No. 1.5e-13;  
RESULT 730  
ID ADM56387 standard; protein; 404 AA.  
DE Human cell adhesion molecule NOV12.  
PN US2003082554-A1.  
PD 01-MAY-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 14.2%; Score 256.5; DB 7; Length 404;  
Best Local Similarity 27.4%; Pred. No. 2.4e-13;  
RESULT 731  
ID AAY33741 standard; protein; 444 AA.  
DE Beta-secretase.  
PN US5942400-A.  
PD 24-AUG-1999.  
PA (ELAN-) ELAN PHARM INC.  
Query Match 14.2%; Score 256; DB 2; Length 444;  
Best Local Similarity 26.7%; Pred. No. 3.1e-13;  
RESULT 732  
ID AAB47251 standard; protein; 444 AA.  
DE Beta-secretase.  
PN US6221645-B1.  
PD 24-APR-2001.  
PA (ELAN-) ELAN PHARM INC.  
Query Match 14.2%; Score 256; DB 4; Length 444;  
Best Local Similarity 26.7%; Pred. No. 3.1e-13;  
RESULT 733  
ID ABB63920 standard; protein; 359 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 18552.  
PN W0200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE-) PE CORP NY.  
Query Match 14.1%; Score 255; DB 4; Length 359;  
Best Local Similarity 24.9%; Pred. No. 2.8e-13;  
RESULT 734  
ID ADN24208 standard; protein; 5175 AA.  
DE Bacterial polypeptide #6861.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 14.1%; Score 254.5; DB 8; Length 5175;  
Best Local Similarity 29.3%; Pred. No. 1.2e-11;  
RESULT 735  
ID ADN24206 standard; protein; 5175 AA.  
DE Bacterial polypeptide #6859.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.

PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 14.1%; Score 254.5; DB 8; Length 5175;  
Best Local Similarity 29.3%; Pred. No. 1.2e-11;  
RESULT 736  
ID ADN24207 standard; protein; 5198 AA.  
DE Bacterial polypeptide #6860.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 14.1%; Score 254.5; DB 8; Length 5198;  
Best Local Similarity 29.3%; Pred. No. 1.2e-11;  
RESULT 737  
ID ADN24205 standard; protein; 5198 AA.  
DE Bacterial polypeptide #6858.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 14.1%; Score 254.5; DB 8; Length 5198;  
Best Local Similarity 29.3%; Pred. No. 1.2e-11;  
RESULT 738  
ID ADM74177 standard; protein; 306 AA.  
DE Human NOV3D protein sequence SeqID16.  
PN WO2004015079-A2.  
PD 19-FEB-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 14.0%; Score 253.5; DB 8; Length 306;  
Best Local Similarity 27.1%; Pred. No. 3e-13;  
RESULT 739  
ID AG66677 standard; protein; 404 AA.  
DE Human novel polypeptide #12.  
PN WO200244340-A2.  
PD 06-JUN-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.0%; Score 253.5; DB 5; Length 404;  
Best Local Similarity 27.1%; Pred. No. 4.4e-13;  
RESULT 740  
ID ABJ20221 standard; protein; 404 AA.  
DE Human IG gene related protein SEQ ID No 44.  
PN WO200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 14.0%; Score 253.5; DB 6; Length 404;  
Best Local Similarity 27.1%; Pred. No. 4.4e-13;  
RESULT 741  
ID ADF66751 standard; protein; 404 AA.  
DE Novel human protein NOV12.  
PN US2003199103-A1.  
PD 23-OCT-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 14.0%; Score 253.5; DB 8; Length 404;  
Best Local Similarity 27.1%; Pred. No. 4.4e-13;  
RESULT 742  
ID ADI19788 standard; protein; 404 AA.  
DE Human NOV12 protein.  
PN US2004002134-A1.  
PD 01-JAN-2004.  
PA (CURA-) CURAGEN CORP.  
Query Match 14.0%; Score 253.5; DB 8; Length 404;  
Best Local Similarity 27.1%; Pred. No. 4.4e-13;  
RESULT 743  
ID ADO60261 standard; protein; 404 AA.  
DE Human NOV12 protein.  
PN US2003134430-A1.  
PD 17-JUL-2003.  
PA (NUVE-) NUVELO.

PA (CURA-) CURAGEN CORP.  
Query Match 14.0%; Score 253.5; DB 8; Length 404;  
Best Local Similarity 27.1%; Pred. No. 4.4e-13;  
RESULT 744  
ID ADO47378 standard; protein; 568 AA.  
DE Human neurotrophin-like protein-related protein SeqID13.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO.  
Query Match 14.0%; Score 253; DB 8; Length 568;  
Best Local Similarity 27.4%; Pred. No. 7.8e-13;  
RESULT 745  
ID ABB76023 standard; protein; 570 AA.  
DE Neurotrophin-like polypeptide.  
PN WO200157175-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.0%; Score 253; DB 4; Length 570;  
Best Local Similarity 27.4%; Pred. No. 7.8e-13;  
RESULT 746  
ID ABB76018 standard; protein; 586 AA.  
DE Neurotrophin-like polypeptide splice variant.  
PN WO200157175-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 14.0%; Score 253; DB 4; Length 586;  
Best Local Similarity 27.4%; Pred. No. 8.1e-13;  
RESULT 747  
ID ADO47372 standard; protein; 586 AA.  
DE Human neurotrophin-like protein SeqID7.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO.  
Query Match 14.0%; Score 253; DB 8; Length 586;  
Best Local Similarity 27.4%; Pred. No. 8.1e-13;  
RESULT 748  
ID ABO23244 standard; protein; 404 AA.  
DE Human breast tumour associated protein 47-like polypeptide NOV12.  
PN US2003027158-A1.  
PD 06-FEB-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.9%; Score 251.5; DB 6; Length 404;  
Best Local Similarity 27.1%; Pred. No. 6.6e-13;  
RESULT 749  
ID AAB61142 standard; protein; 404 AA.  
DE Human NOV12 protein.  
PN WO200075321-A2.  
PD 14-DEC-2000.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.9%; Score 250.5; DB 4; Length 404;  
Best Local Similarity 27.1%; Pred. No. 8e-13;  
RESULT 750  
ID ABB61502 standard; protein; 885 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 11298.  
PN WO200171042-A2.  
PD 27-SEP-2001.  
PA (PEKE) PE CORP NY.  
Query Match 13.9%; Score 250.5; DB 4; Length 885;  
Best Local Similarity 26.5%; Pred. No. 2.3e-12;  
RESULT 751  
ID ABB76016 standard; protein; 374 AA.  
DE Neurotrophin-like polypeptide.  
PN WO200157175-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.8%; Score 250; DB 4; Length 374;  
Best Local Similarity 27.7%; Pred. No. 8e-13;  
RESULT 752  
ID ADO47381 standard; protein; 374 AA.  
DE Human neurotrophin-like protein-related protein SeqID16.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO.

Query Match 13.8%; Score 250; DB 8; Length 374;  
Best Local Similarity 27.7%; Pred. No. 8e-13;  
RESULT 753  
ID ADO47377 standard; protein; 440 AA.  
DE Human neurotrophin-like protein-related protein SeqID12.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO.  
Query Match 13.8%; Score 250; DB 8; Length 440;  
Best Local Similarity 27.7%; Pred. No. 9.9e-13;  
RESULT 754  
ID ABE76022 standard; protein; 442 AA.  
DE Neurotrophin-like polypeptide.  
PN WO200157175-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.8%; Score 250; DB 4; Length 442;  
Best Local Similarity 27.7%; Pred. No. 1e-12;  
RESULT 755  
ID ABB76017 standard; protein; 458 AA.  
DE Neurotrophin-like polypeptide.  
PN WO200157175-A2.  
PD 09-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.8%; Score 250; DB 4; Length 458;  
Best Local Similarity 27.7%; Pred. No. 1e-12;  
RESULT 756  
ID ADO47369 standard; protein; 458 AA.  
DE Human neurotrophin-like protein SeqID4.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO.  
Query Match 13.8%; Score 250; DB 8; Length 458;  
Best Local Similarity 27.7%; Pred. No. 1e-12;  
RESULT 757  
ID ADS10607 standard; protein; 458 AA.  
DE Human therapeutic protein - SEQ ID 844.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 13.8%; Score 250; DB 8; Length 458;  
Best Local Similarity 27.7%; Pred. No. 1e-12;  
RESULT 758  
ID ADO47385 standard; protein; 880 AA.  
DE Human neurotrophin-like protein-related protein SeqID13.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO.  
Query Match 13.8%; Score 250; DB 8; Length 880;  
Best Local Similarity 27.7%; Pred. No. 2.6e-12;  
RESULT 759  
ID AAO30844 standard; protein; 886 AA.  
DE Human cell adhesion and extracellular matrix protein (CADECM) -34.  
PN WO2003047526-A2.  
PD 12-JUN-2003.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 13.8%; Score 250; DB 7; Length 886;  
Best Local Similarity 27.7%; Pred. No. 2.6e-12;  
RESULT 760  
ID ADO47396 standard; protein; 955 AA.  
DE Human neurotrophin-like protein-related MAM domain GPIM protein SeqID31.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO.  
Query Match 13.8%; Score 250; DB 8; Length 955;  
Best Local Similarity 27.7%; Pred. No. 2.9e-12;  
RESULT 761  
ID ADO47383 standard; protein; 955 AA.  
DE Human neurotrophin-like protein SeqID18.  
PN WO2004039942-A2.  
PD 13-MAY-2004.  
PA (NUVE-) NUVELO.  
Query Match 13.8%; Score 250; DB 8; Length 955;  
Best Local Similarity 27.7%; Pred. No. 2.9e-12;  
RESULT 762  
ID ADS10608 standard; protein; 955 AA.  
DE Human therapeutic protein - SEQ ID 845.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 13.8%; Score 250; DB 8; Length 955;  
Best Local Similarity 27.7%; Pred. No. 2.9e-12;  
RESULT 763  
ID ADS11107 standard; protein; 970 AA.  
DE Human therapeutic protein - SEQ ID 1344.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 13.8%; Score 250; DB 8; Length 970;  
Best Local Similarity 27.7%; Pred. No. 2.9e-12;  
RESULT 764  
ID ABG12100 standard; protein; 1219 AA.  
DE Novel human diagnostic protein #12091.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.8%; Score 250; DB 4; Length 1219;  
Best Local Similarity 27.7%; Pred. No. 4e-12;  
RESULT 765  
ID ABUS2336 standard; protein; 1315 AA.  
DE Human GPCR related protein NOV13a.  
PN WO200279398-A2.  
PD 10-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.8%; Score 250; DB 6; Length 1315;  
Best Local Similarity 27.7%; Pred. No. 4.4e-12;  
RESULT 766  
ID ADH72138 standard; protein; 1315 AA.  
DE Human protein of the invention NOV46h SEQ ID NO:1034.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.8%; Score 250; DB 8; Length 1315;  
Best Local Similarity 27.7%; Pred. No. 4.4e-12;  
RESULT 767  
ID ADL24007 standard; protein; 1315 AA.  
DE Human NOVX polypeptide #26.  
PN US2004002120-A1.  
PD 01-JAN-2004.  
PA (KEKU/) KEKUDA R.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (PATT/) PATTURAJAN M.  
PA (BURG/) BURGESS C E.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (GORM/) GORMAN L.  
PA (MALY/) MALYANKAR U M.  
PA (BOLD/) BOLDOG F L.  
PA (GUOX/) GUO X.  
PA (SHEN/) SHENOY S G.  
PA (PADI/) PADIGAR R M.  
PA (TAUP/) TAUPIER R J.  
PA (MILL/) MILLER C E.  
PA (CASM/) CASHMAN S J.  
PA (PENA/) PENA C E A.  
PA (GANG/) GANGOLLI E A.  
PA (GUSE/) GUSEV V Y.  
PA (SMIT/) SMITHSON G.  
PA (ZERH/) ZERHUSEN B D.  
PA (GERL/) GERLACH V.  
PA (POCH/) POCHART P F.  
PA (FERN/) FERNANDES E R.  
PA (SHIM/) SHIMKETS R A.  
PA (RAST/) RASTELLI L.

PA (SPAD/) SPADERNA S K. 13.8%; Score 250; DB 8; Length 1315;  
PA (LARO/) LAROCHELLE W J. 27.7%; Pred. No. 4.4e-12;  
PA (ZHON/) ZHONG M.  
PA (KHRA/) KHRAMTSOV N V.  
PA (VOSS/) VOSS E Z.  
PA (HERR/) HERRMANN J L.  
Query Match 13.8%; Score 250; DB 8; Length 1315;  
Best Local Similarity 27.7%; Pred. No. 4.4e-12;  
RESULT 768  
ID ADH72134 standard; protein; 1335 AA.  
DE Human protein of the invention NOV46f SEQ ID NO:1030.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.8%; Score 250; DB 8; Length 1335;  
Best Local Similarity 27.7%; Pred. No. 4.5e-12;  
RESULT 769  
ID ABU52329 standard; protein; 1386 AA.  
DE Human GPCR related protein NOV12a.  
PN WO200279398-A2.  
PD 10-OCT-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.8%; Score 250; DB 6; Length 1386;  
Best Local Similarity 27.7%; Pred. No. 4.8e-12;  
RESULT 770  
ID ADL23993 standard; protein; 1386 AA.  
DE Human NOVX polypeptide #19.  
PN US2004002120-A1.  
PD 01-JAN-2004.  
PA (KEKU/) KEKUDA R.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (PATT/) PATTURAJAN M.  
PA (BURG/) BURGESS C E.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (GORM/) GORMAN L.  
PA (MALY/) MALYANKAR U M.  
PA (BOLD/) BOLDOG F L.  
PA (GUOX/) GUO X.  
PA (SHEN/) SHENOY S G.  
PA (PADI/) PADIGARU M.  
PA (TAUP/) TAUFIER R J.  
PA (MILL/) MILLER C E.  
PA (CASM/) CASMAN S J.  
PA (PENA/) PENNA C E A.  
PA (GANG/) GANGOLLI E A.  
PA (GUSE/) GUSEV V Y.  
PA (SMIT/) SMITHSON G.  
PA (ZERH/) ZERHUSEN B D.  
PA (GERL/) GERLACH V.  
PA (POCH/) POCHART P F.  
PA (FERN/) FERNANDES E R.  
PA (SHIM/) SHIMKETS R A.  
PA (RAST/) RASTELLI L.  
PA (SPAD/) SPADERNA S K.  
PA (LARO/) LAROCHELLE W J.  
PA (ZHON/) ZHONG M.  
PA (KHRA/) KHRAMTSOV N V.  
PA (VOSS/) VOSS E Z.  
PA (HERR/) HERRMANN J L.  
Query Match 13.8%; Score 250; DB 8; Length 1386;  
Best Local Similarity 27.7%; Pred. No. 4.8e-12;  
RESULT 771  
ID ADD47172 standard; protein; 1040 AA.  
DE Human Protein NP\_005067, SEQ ID NO 12866.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO/) GEN HOSPITAL CORP.  
PA (FARB/) BAYER AG.  
Query Match 13.8%; Score 249.5; DB 7; Length 1040;  
Best Local Similarity 26.1%; Pred. No. 3.6e-12;  
RESULT 772  
ID ADO28581 standard; protein; 1040 AA.  
DE Human axonin-1 precursor (AXO1) protein SEQ ID NO:10.  
PN WO2004044178-A2.  
PD 27-MAY-2004.  
PA (GETH/) GENENTECH INC.  
Query Match 13.8%; Score 249.5; DB 8; Length 1040;  
Best Local Similarity 26.1%; Pred. No. 3.6e-12;  
RESULT 773  
ID ABO84729 standard; protein; 1040 AA.  
DE Human cancer-associated protein HP22-025.2.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 13.8%; Score 249.5; DB 8; Length 1040;  
Best Local Similarity 26.1%; Pred. No. 3.6e-12;  
RESULT 774  
ID ABO84728 standard; protein; 1040 AA.  
DE Human cancer-associated protein HP22-025.1.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 13.8%; Score 249.5; DB 8; Length 1040;  
Best Local Similarity 26.1%; Pred. No. 3.6e-12;  
RESULT 775  
ID ABB68882 standard; protein; 467 AA.  
DE Drosophila melanogaster polypeptide SEQ ID NO 33438.  
PN WO200171042-A2.  
PD 27-SBP-2001.  
PA (PEKE/) PE CORP NY.  
Query Match 13.7%; Score 248; DB 4; Length 467;  
Best Local Similarity 27.4%; Pred. No. 1.6e-12;  
RESULT 776  
ID ADJ68312 standard; protein; 1007 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID118.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 13.6%; Score 246.5; DB 7; Length 1007;  
Best Local Similarity 24.6%; Pred. No. 6.2e-12;  
RESULT 777  
ID AAR63759 standard; protein; 1018 AA.  
DE Human contactin (EMBL Accession #Z21488).  
PN EP618293-A1.  
PD 05-OCT-1994.  
PA (BECT/) BECTON DICKINSON CO.  
Query Match 13.6%; Score 246.5; DB 2; Length 1018;  
Best Local Similarity 24.6%; Pred. No. 6.3e-12;  
RESULT 778  
ID AAR87028 standard; protein; 1018 AA.  
DE Human contactin.  
PN WO9535373-A2.  
PD 28-DEC-1995.  
PA (LJOL-) LA JOLLA CANCER RES FOUND.  
Query Match 13.6%; Score 246.5; DB 2; Length 1018;  
Best Local Similarity 24.6%; Pred. No. 6.3e-12;  
RESULT 779  
ID ADE71113 standard; protein; 1018 AA.  
DE Contactin, SEQ ID 67.  
PN WO2003070889-A2.  
PD 28-AUG-2003.  
PA (IDEC-) IDEC PHARM CORP.  
Query Match 13.8%; Score 246.5; DB 7; Length 1018;  
Best Local Similarity 24.6%; Pred. No. 6.3e-12;  
RESULT 780  
ID ADJ75696 standard; protein; 1018 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:948.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 13.6%; Score 246.5; DB 8; Length 1018;  
Best Local Similarity 24.6%; Pred. No. 6.3e-12;

RESULT 781  
ID AD028659 standard; protein; 1018 AA.  
DE Human CONT protein SEQ ID NO:88.  
PN WO2004044178-A2.  
PD 27-MAY-2004.  
PA (GETH) GENENTECH INC.  
Query Match 13.6%; Score 246.5; DB 8; Length 1018;  
Best Local Similarity 24.6%; Pred. No. 6.3e-12;  
RESULT 782  
ID ADP67246 standard; protein; 1018 AA.  
DE Human F3/Contactin protein.  
PN WO2004052389-A2.  
PD 24-JUN-2004.  
PA (SIGE-) SINGAPORE GEN HOSPITAL PTE LTD.  
PA (FORR-) FORREST G R.  
Query Match 13.6%; Score 246.5; DB 8; Length 1018;  
Best Local Similarity 24.6%; Pred. No. 6.3e-12;  
RESULT 783  
ID ADR66068 standard; protein; 1073 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 264 #1.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ-) HINZMANN B.  
PA (DAHL-) DAHL E.  
PA (ROSE-) ROSENTHAL A.  
PA (HERM-) HERMANN K.  
PA (PILA-) PILARSKY C.  
Query Match 13.6%; Score 245.5; DB 8; Length 1073;  
Best Local Similarity 26.4%; Pred. No. 8.2e-12;  
RESULT 784  
ID ADR66410 standard; protein; 1073 AA.  
DE Human prostatic carcinoma derived protein SEQ ID 264 #2.  
PN WO2004076614-A2.  
PD 10-SEP-2004.  
PA (HINZ-) HINZMANN B.  
PA (DAHL-) DAHL E.  
PA (ROSE-) ROSENTHAL A.  
PA (HERM-) HERMANN K.  
PA (PILA-) PILARSKY C.  
Query Match 13.6%; Score 245.5; DB 8; Length 1073;  
Best Local Similarity 26.4%; Pred. No. 8.2e-12;  
RESULT 785  
ID ADA54925 standard; protein; 512 AA.  
DE Human protein, SEQ ID 2493.  
PN EPI293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 13.5%; Score 244.5; DB 6; Length 512;  
Best Local Similarity 27.8%; Pred. No. 3.6e-12;  
RESULT 786  
ID AAW06485 standard; peptide; 1018 AA.  
DE Rat contactin ligand for RPTbeta.  
PN W09637776-A1.  
PD 28-NOV-1996.  
PA (SUGE-) SUGEN INC.  
Query Match 13.5%; Score 243.5; DB 2; Length 1018;  
Best Local Similarity 24.0%; Pred. No. 1.1e-11;  
RESULT 787  
ID ADE56173 standard; protein; 1021 AA.  
DE Rat Protein Q63198, SEQ ID NO 2022.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GHEO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 13.5%; Score 243.5; DB 7; Length 1021;  
Best Local Similarity 24.0%; Pred. No. 1.1e-11;  
RESULT 788  
ID ABO30059 standard; protein; 792 AA.  
DE Novel human diagnostic protein #3050.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.

Query Match 13.4%; Score 242.5; DB 4; Length 792;  
Best Local Similarity 26.4%; Pred. No. 9.8e-12;  
RESULT 789  
ID ABG00258 standard; protein; 893 AA.  
DE Novel human diagnostic protein #249.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.4%; Score 242.5; DB 4; Length 893;  
Best Local Similarity 26.4%; Pred. No. 1.2e-11;  
RESULT 790  
ID ABG00611 standard; protein; 893 AA.  
DE Novel human diagnostic protein #602.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.4%; Score 242.5; DB 4; Length 893;  
Best Local Similarity 26.4%; Pred. No. 1.2e-11;  
RESULT 791  
ID ABG31317 standard; protein; 2586 AA.  
DE Human 5+3 corrected OCP protein.  
PN WO200246364-A2.  
PD 13-JUN-2002.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 13.4%; Score 242; DB 5; Length 2586;  
Best Local Similarity 27.0%; Pred. No. 5.5e-11;  
RESULT 792  
ID ABG32891 standard; protein; 2586 AA.  
DE Human osteoclast protein (OCP) #1.  
PN US2002086825-A1.  
PD 04-JUL-2002.  
PA (EINA/) EINAT P.  
PA (SEGE/) SEGEV O.  
PA (SKAL/) SKALITER R.  
PA (FEIN/) FEINSTEIN E.  
PA (FAER/) FAERMAN A.  
Query Match 13.4%; Score 242; DB 5; Length 2586;  
Best Local Similarity 27.0%; Pred. No. 5.5e-11;  
RESULT 793  
ID ADL02231 standard; protein; 2586 AA.  
DE Human OCP protein #1.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 13.4%; Score 242; DB 8; Length 2586;  
Best Local Similarity 27.0%; Pred. No. 5.5e-11;  
RESULT 794  
ID ADL02234 standard; protein; 2586 AA.  
DE Human OCP protein #2.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 13.4%; Score 242; DB 8; Length 2586;  
Best Local Similarity 27.0%; Pred. No. 5.5e-11;  
RESULT 795  
ID AAB47935 standard; protein; 2587 AA.  
DE Human OCP.  
PN US2002022026-A1.  
PD 21-FEB-2002.  
PA (EINA/) EINAT P.  
PA (SEGE/) SEGEV O.  
PA (SKAL/) SKALITER R.  
PA (FEIN/) FEINSTEIN E.  
PA (FAER/) FAERMAN A.  
Query Match 13.4%; Score 242; DB 5; Length 2587;  
Best Local Similarity 27.0%; Pred. No. 5.5e-11;  
RESULT 796  
ID ABG32896 standard; protein; 2587 AA.  
DE Human osteoclast protein (OCP) #2.  
PN US2002086825-A1.  
PD 04-JUL-2002.  
PA (EINA/) EINAT P.  
PA (SEGE/) SEGEV O.

PA (SKAL/) SKALITER R.  
PA (FEIN/) FEINSTEIN E.  
PA (FAER/) FAERMAN A.  
Query Match 13.4%; Score 242; DB 5; Length 2587;  
Best Local Similarity 27.0%; Pred. No. 5.5e-11;  
RESULT 797  
ID ADL02236 standard; protein; 2587 AA.  
DE Human OCP protein #3.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 13.4%; Score 242; DB 8; Length 2587;  
Best Local Similarity 27.0%; Pred. No. 5.5e-11;  
RESULT 798  
ID AEG31323 standard; protein; 2589 AA.  
DE Human OCP protein.  
PN WO200246364-A2.  
PD 13-JUN-2002.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 13.4%; Score 242; DB 5; Length 2589;  
Best Local Similarity 27.0%; Pred. No. 5.5e-11;  
RESULT 799  
ID ADL02244 standard; protein; 2589 AA.  
DE Human OCP protein #5.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 13.4%; Score 242; DB 8; Length 2589;  
Best Local Similarity 27.0%; Pred. No. 5.5e-11;  
RESULT 800  
ID AAR92256 standard; protein; 582 AA.  
DE Neural cell adhesion molecule splice variant.  
PN WO9604396-A1.  
PD 15-FEB-1996.  
PA (SYST-) SYSTEMIX INC.  
Query Match 13.4%; Score 241.5; DB 2; Length 582;  
Best Local Similarity 24.4%; Pred. No. 7.9e-12;  
RESULT 801  
ID AAR92255 standard; protein; 761 AA.  
DE Neural cell adhesion molecule.  
PN WO9604396-A1.  
PD 15-FEB-1996.  
PA (SYST-) SYSTEMIX INC.  
Query Match 13.4%; Score 241.5; DB 2; Length 761;  
Best Local Similarity 24.4%; Pred. No. 1.1e-11;  
RESULT 802  
ID ADI24547 standard; protein; 837 AA.  
DE Human modifier of Chk1 (MCHK) protein SEQ ID NO:97.  
PN WO2004004785-A1.  
PD 15-JAN-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match 13.4%; Score 241.5; DB 8; Length 837;  
Best Local Similarity 24.7%; Pred. No. 1.3e-11;  
RESULT 803  
ID ADJ76385 standard; protein; 1020 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:1637.  
PN EP1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 13.4%; Score 241.5; DB 8; Length 1020;  
Best Local Similarity 24.3%; Pred. No. 1.7e-11;  
RESULT 804  
ID ABO07536 standard; protein; 891 AA.  
DE Novel human diagnostic protein #7527.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.3%; Score 241; DB 4; Length 891;  
Best Local Similarity 45.7%; Pred. No. 1.6e-11;  
RESULT 805  
ID ABP69251 standard; protein; 2173 AA.  
DE Human polypeptide SEQ ID NO 1298.  
PN WO200270539-A2.

PD 12-SEP-2002.  
PA (HYSE-) HYSEQ INC.  
Query Match 13.3%; Score 241; DB 5; Length 2173;  
Best Local Similarity 26.7%; Pred. No. 5.3e-11;  
RESULT 806  
ID AAE00585 standard; protein; 793 AA.  
DE Human nuclear cell adhesion molecule homologue, NCAM\_c\_1 protein.  
PN WO200129215-A2.  
PD 26-APR-2001.  
PA (COMP-) COMPUGEN LTD.  
Query Match 13.2%; Score 238.5; DB 4; Length 793;  
Best Local Similarity 25.4%; Pred. No. 2.2e-11;  
RESULT 807  
ID AAE00584 standard; protein; 848 AA.  
DE Human nuclear cell adhesion molecule homologue, NCAM\_c\_2 protein.  
PN WO200129215-A2.  
PD 26-APR-2001.  
PA (COMP-) COMPUGEN LTD.  
Query Match 13.2%; Score 238.5; DB 4; Length 848;  
Best Local Similarity 25.4%; Pred. No. 2.4e-11;  
RESULT 808  
ID AAE00586 standard; protein; 891 AA.  
DE Human nuclear cell adhesion molecule homologue, NCAM\_d\_2 protein.  
PN WO200129215-A2.  
PD 26-APR-2001.  
PA (COMP-) COMPUGEN LTD.  
Query Match 13.2%; Score 238.5; DB 4; Length 891;  
Best Local Similarity 25.4%; Pred. No. 2.6e-11;  
RESULT 809  
ID AAE00583 standard; protein; 920 AA.  
DE Human cell adhesion molecule homologue (CAM-H) protein #2.  
PN WO200129215-A2.  
PD 26-APR-2001.  
PA (COMP-) COMPUGEN LTD.  
Query Match 13.2%; Score 238.5; DB 4; Length 920;  
Best Local Similarity 25.4%; Pred. No. 2.7e-11;  
RESULT 810  
ID AAE00582 standard; protein; 946 AA.  
DE Human nuclear cell adhesion molecule homologue, NCAM\_d\_1 protein.  
PN WO200129215-A2.  
PD 26-APR-2001.  
PA (COMP-) COMPUGEN LTD.  
Query Match 13.2%; Score 238.5; DB 4; Length 946;  
Best Local Similarity 25.4%; Pred. No. 2.8e-11;  
RESULT 811  
ID AAE00581 standard; protein; 1018 AA.  
DE Human cell adhesion molecule homologue (CAM-H) protein #1.  
PN WO200129215-A2.  
PD 26-APR-2001.  
PA (COMP-) COMPUGEN LTD.  
Query Match 13.2%; Score 238.5; DB 4; Length 1018;  
Best Local Similarity 25.4%; Pred. No. 3.1e-11;  
RESULT 812  
ID AAW05161 standard; protein; 73 AA.  
DE Human LAMP residues 46-118.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 13.1%; Score 237; DB 2; Length 73;  
Best Local Similarity 58.3%; Pred. No. 1.1e-12;  
RESULT 813  
ID AAW05162 standard; protein; 73 AA.  
DE Rat LAMP residues 46-118.  
PN WO9630052-A1.  
PD 03-OCT-1996.  
PA (UMDN-) UMDNJ UNIV NEW JERSEYS HEALTH SCI.  
Query Match 13.1%; Score 237; DB 2; Length 73;  
Best Local Similarity 58.3%; Pred. No. 1.1e-12;  
RESULT 814  
ID ADR09877 standard; protein; 632 AA.  
DE Human protein useful for treating neurological disease Seq 3383.  
PN EP1447413-A2.  
PD 18-AUG-2004.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 13.0%; Score 235.5; DB 8; Length 632;  
Best Local Similarity 26.9%; Pred. No. 2.9e-11;  
RESULT 815  
ID ADH71818 standard; protein; 967 AA.  
DE Human protein of the invention NOV29y SEQ ID NO:714.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 13.0%; Score 235.5; DB 8; Length 967;  
Best Local Similarity 27.1%; Pred. No. 5.2e-11;  
RESULT 816  
ID ADS10576 standard; protein; 2428 AA.  
DE Human therapeutic protein - SEQ ID 813.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 13.0%; Score 235.5; DB 8; Length 2428;  
Best Local Similarity 26.9%; Pred. No. 1.8e-10;  
RESULT 817  
ID ADL02252 standard; protein; 2623 AA.  
DE Human OCP protein #7.  
PN US2004053301-A1.  
PD 18-MAR-2004.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 13.0%; Score 235.5; DB 8; Length 2623;  
Best Local Similarity 26.9%; Pred. No. 2e-10;  
RESULT 818  
ID ADS10577 standard; protein; 2623 AA.  
DE Human therapeutic protein - SEQ ID 814.  
PN WO2004080148-A2.  
PD 23-SEP-2004.  
PA (NUVE-) NUVELO INC.  
Query Match 13.0%; Score 235.5; DB 8; Length 2623;  
Best Local Similarity 26.9%; Pred. No. 2e-10;  
RESULT 819  
ID ADN24073 standard; protein; 662 AA.  
DE Bacterial polypeptide #6726.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 13.0%; Score 235; DB 8; Length 662;  
Best Local Similarity 25.5%; Pred. No. 3.4e-11;  
RESULT 820  
ID ADD47171 standard; protein; 1040 AA.  
DE Rat Protein AAA42201, SEQ ID NO 12864.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 13.0%; Score 234.5; DB 7; Length 1040;  
Best Local Similarity 25.8%; Pred. No. 7e-11;  
RESULT 821  
ID ADR67266 standard; protein; 1100 AA.  
DE Human bladder cancer associated amino acid sequence.  
PN WO2004076613-A2.  
PD 10-SEP-2004.  
PA (HERR/) HERR A.  
PA (HINZ/) HINZMANN B.  
PA (DAHL/) DAHL E.  
PA (STAU/) STAUB E.  
PA (PILA/) PILARSKY C.  
PA (SPEC/) SPECHT T.  
Query Match 12.9%; Score 233.5; DB 8; Length 1100;  
Best Local Similarity 24.9%; Pred. No. 9.2e-11;  
RESULT 822  
ID ADH71816 standard; protein; 967 AA.  
DE Human protein of the invention NOV29x SEQ ID NO:712.  
PN WO2003102155-A2.

PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.9%; Score 232.5; DB 8; Length 967;  
Best Local Similarity 26.8%; Pred. No. 9.4e-11;  
RESULT 823  
ID ADN23691 standard; protein; 2783 AA.  
DE Bacterial polypeptide #6344.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.9%; Score 232.5; DB 8; Length 2783;  
Best Local Similarity 23.5%; Pred. No. 4e-10;  
RESULT 824  
ID ABG69614 standard; protein; 2401 AA.  
DE Human NOV12a protein.  
PN WO200250277-A2.  
PD 27-JUN-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.8%; Score 232; DB 5; Length 2401;  
Best Local Similarity 26.9%; Pred. No. 3.6e-10;  
RESULT 825  
ID ABG69619 standard; protein; 2447 AA.  
DE Human NOV12f protein.  
PN WO200250277-A2.  
PD 27-JUN-2002.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.8%; Score 232; DB 5; Length 2447;  
Best Local Similarity 26.9%; Pred. No. 3.7e-10;  
RESULT 826  
ID ADJ83065 standard; protein; 2591 AA.  
DE Human NOVX NOV12f protein.  
PN US2003170630-A1.  
PD 11-SEP-2003.  
PA (ALSO/) ALSOBROOK J P.  
PA (TCHE/) TCHERNEV V T.  
PA (LIUX/) LIU X.  
PA (SPYT/) SPYTEK K A.  
PA (ZERH/) ZERHUSEN B D.  
PA (PATT/) PATTURAJAN M.  
PA (LEPL/) LEPLY D M.  
PA (BURG/) BURGESS C E.  
PA (SHIM/) SHINKETS R A.  
PA (GROS/) GROSSE W M.  
PA (SZEK/) SZEKERES E S.  
PA (VERN/) VERNET C A M.  
PA (LILL/) LI L.  
PA (CASM/) CASMAN S J.  
PA (BOLD/) BOLDOG F L.  
PA (GORM/) GORMAN L.  
PA (GANG/) GANGOLLI E A.  
PA (FERN/) FERNANDES E R.  
PA (RIEG/) RIEGER D K.  
PA (EDIN/) EDINGER S R.  
PA (GUNT/) GUNTHER E.  
PA (MILL/) MILLET I.  
PA (SCIO/) SCIORE P.  
PA (ELLE/) ELLERMAN K.  
PA (MACD/) MACDOUGALL J R.  
PA (SMIT/) SMITHSON G.  
Query Match 12.8%; Score 232; DB 7; Length 2591;  
Best Local Similarity 26.9%; Pred. No. 4e-10;  
RESULT 827  
ID ADH71822 standard; protein; 2591 AA.  
DE Human protein of the invention NOV29aa SEQ ID NO:718.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.8%; Score 232; DB 8; Length 2591;  
Best Local Similarity 26.9%; Pred. No. 4e-10;



```
RESULT 828
ID ADH71820 standard; protein; 2602 AA.
DE Human protein of the invention NOV29z SEQ ID NO:716.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2602;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 829
ID ADJ83055 standard; protein; 2617 AA.
DE Human NOVX NOV12a protein.
PN US2003170630-A1.
PD 11-SEP-2003.
PA (ALSO/) ALSOBROOK J P.
PA (TCHE/) TCHERNEV V T.
PA (LIUX/) LIU X.
PA (SPYT/) SPYTEK K A.
PA (ZERH/) ZERHUSEN B D.
PA (PATY/) PATTURAJAN M.
PA (LEPL/) LEPLEY D M.
PA (BURG/) BURGESS C E.
PA (SHIM/) SHIMKETS R A.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (VERN/) VERNET C A M.
PA (LILL/) LI L.
PA (CASM/) CASMAN S J.
PA (BOLD/) BOLDOG F L.
PA (GORM/) GORMAN L.
PA (GANG/) GANGOLLI E A.
PA (FERN/) FERNANDES E R.
PA (RIEG/) RIEGER D K.
PA (EDIN/) EDINGER S R.
PA (GUNT/) GUNTHER E.
PA (MILL/) MILLET I.
PA (SCIO/) SCIORE P.
PA (ELLE/) ELLERMAN K.
PA (MACD/) MACDOUGALL J R.
PA (SMIT/) SMITHSON G.
Query Match 12.8%; Score 232; DB 7; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 830
ID ADH71842 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ak SEQ ID NO:738.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 831
ID ADH71852 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ap SEQ ID NO:748.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 832
ID ADH71838 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ai SEQ ID NO:734.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 833
ID ADH71770 standard; protein; 2617 AA.
DE Human protein of the invention NOV29a SEQ ID NO:666.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 834
ID ADH71836 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ah SEQ ID NO:732.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 835
ID ADH71840 standard; protein; 2617 AA.
DE Human protein of the invention NOV29aj SEQ ID NO:736.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 836
ID ADH71844 standard; protein; 2617 AA.
DE Human protein of the invention NOV29al SEQ ID NO:740.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 837
ID ADH71846 standard; protein; 2617 AA.
DE Human protein of the invention NOV29am SEQ ID NO:742.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 838
ID ADH71850 standard; protein; 2617 AA.
DE Human protein of the invention NOV29ao SEQ ID NO:746.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 839
ID ADH71854 standard; protein; 2617 AA.
DE Human protein of the invention NOV29aq SEQ ID NO:750.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 840
ID ADH71848 standard; protein; 2617 AA.
DE Human protein of the invention NOV29an SEQ ID NO:744.
PN WO2003102155-A2.
PD 11-DEC-2003.
PA (CURA-) CURAGEN CORP.
Query Match 12.8%; Score 232; DB 8; Length 2617;
Best Local Similarity 26.9%; Pred. No. 4.1e-10;
RESULT 841
ID AEU07377 standard; protein; 3931 AA.
DE Human protein NOV9.
PN WO200285922-A2.
PD 31-OCT-2002.
PA (CURA-) CURAGEN CORP.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 12.8%; Score 232; DB 6; Length 3931;
Best Local Similarity 28.3%; Pred. No. 7.1e-10;
RESULT 842
ID AAW29667 standard; protein; 1028 AA.
DE Homo sapiens DL185_1 clone secreted protein.
PN WO9830695-A2.
PD 16-JUL-1998.
PA (GEMY) GENETICS INST INC.
Query Match 12.8%; Score 231; DB 2; Length 1028;
Best Local Similarity 26.7%; Pred. No. 1.4e-10;
```

RESULT 843  
ID ADP67247 standard; protein; 1028 AA.  
DE Human NB-3 protein.  
PN WO2004052389-A2.  
PD 24-JUN-2004.  
PA (SAGE-) SINGAPORE GEN HOSPITAL PTE LTD.  
PA (FORR-) FORREST G R.  
Query Match 12.8%; Score 231; DB 8; Length 1028;  
Best Local Similarity 26.7%; Pred. No. 1.4e-10;  
RESULT 844  
ID ADG39786 standard; protein; 3931 AA.  
DE Human novel protein NOV9.  
PN US2003203843-A1.  
PD 30-OCT-2003.  
PA (PENA/) PENA C E A.  
PA (GUOX/) GUO X.  
PA (SHIM/) SHIMKETS R A.  
PA (PADI/) PADIGARU M.  
PA (KEKU/) KEKUDA R.  
PA (SPYT/) SPYTEK K A.  
PA (MEHR/) MEHRABAN F.  
PA (TOPP/) TOPPER J N.  
PA (MALY/) MALYANKAR U M.  
PA (WASS/) WASSERMAN S M.  
PA (EDIN/) EDINGER S R.  
PA (SMIT/) SMITHSON G.  
PA (GUNT/) GUNTHER E.  
PA (KOMU/) KOMUVES L.  
Query Match 12.8%; Score 231; DB 7; Length 3931;  
Best Local Similarity 28.3%; Pred. No. 8.6e-10;  
RESULT 845  
ID AAW26507 standard; protein; 868 AA.  
DE Rat Dmk receptor.  
PN US5656473-A.  
PD 12-AUG-1997.  
PA (REGE-) REGENERON PHARM INC.  
Query Match 12.8%; Score 230.5; DB 2; Length 868;  
Best Local Similarity 25.2%; Pred. No. 1.2e-10;  
RESULT 846  
ID AAW26610 standard; protein; 868 AA.  
DE Rat muscle-specific kinase (MUSK).  
PN WO9721811-A2.  
PD 19-JUN-1997.  
PA (REGE-) REGENERON PHARM INC.  
Query Match 12.8%; Score 230.5; DB 2; Length 868;  
Best Local Similarity 25.2%; Pred. No. 1.2e-10;  
RESULT 847  
ID ADH71830 standard; protein; 961 AA.  
DE Human protein of the invention NOV29ae SEQ ID NO:726.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.8%; Score 230.5; DB 8; Length 961;  
Best Local Similarity 27.2%; Pred. No. 1.4e-10;  
RESULT 848  
ID ADH71832 standard; protein; 961 AA.  
DE Human protein of the invention NOV29af SEQ ID NO:728.  
PN WO2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.8%; Score 230.5; DB 8; Length 961;  
Best Local Similarity 27.2%; Pred. No. 1.4e-10;  
RESULT 849  
ID ABO84727 standard; protein; 1040 AA.  
DE Mouse cancer-associated protein MP22-025.1.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 12.8%; Score 230.5; DB 8; Length 1040;  
Best Local Similarity 25.0%; Pred. No. 1.5e-10;  
RESULT 850  
ID ABO84469 standard; protein; 3475 AA.  
DE Human cancer-associated protein HP13-036.1.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 12.8%; Score 230.5; DB 8; Length 3475;  
Best Local Similarity 24.3%; Pred. No. 8.1e-10;  
RESULT 851  
ID ADG39842 standard; protein; 1928 AA.  
DE Protein similar to human NOV9 #3.  
PN US2003203843-A1.  
PD 30-OCT-2003.  
PA (PENA/) PENA C E A.  
PA (GUOX/) GUO X.  
PA (SHIM/) SHIMKETS R A.  
PA (PADI/) PADIGARU M.  
PA (KEKU/) KEKUDA R.  
PA (SPYT/) SPYTEK K A.  
PA (MEHR/) MEHRABAN F.  
PA (TOPP/) TOPPER J N.  
PA (MALY/) MALYANKAR U M.  
PA (WASS/) WASSERMAN S M.  
PA (EDIN/) EDINGER S R.  
PA (SMIT/) SMITHSON G.  
PA (GUNT/) GUNTHER E.  
PA (KOMU/) KOMUVES L.  
Query Match 12.7%; Score 230; DB 7; Length 1928;  
Best Local Similarity 22.9%; Pred. No. 4e-10;  
RESULT 852  
ID ADG39843 standard; protein; 1951 AA.  
DE Protein similar to human NOV9 #4.  
PN US2003203843-A1.  
PD 30-OCT-2003.  
PA (PENA/) PENA C E A.  
PA (GUOX/) GUO X.  
PA (SHIM/) SHIMKETS R A.  
PA (PADI/) PADIGARU M.  
PA (KEKU/) KEKUDA R.  
PA (SPYT/) SPYTEK K A.  
PA (MEHR/) MEHRABAN F.  
PA (TOPP/) TOPPER J N.  
PA (MALY/) MALYANKAR U M.  
PA (WASS/) WASSERMAN S M.  
PA (EDIN/) EDINGER S R.  
PA (SMIT/) SMITHSON G.  
PA (GUNT/) GUNTHER E.  
PA (KOMU/) KOMUVES L.  
Query Match 12.7%; Score 230; DB 7; Length 1951;  
Best Local Similarity 22.9%; Pred. No. 4e-10;  
RESULT 853  
ID AAY53667 standard; protein; 3117 AA.  
DE Sequence gi/3328186 from an alignment with protein 608.  
PN WO960164-A1.  
PD 25-NOV-1999.  
PA (QUAR-) QUARK BIOTECH INC.  
Query Match 12.7%; Score 230; DB 3; Length 3117;  
Best Local Similarity 22.9%; Pred. No. 7.7e-10;  
RESULT 854  
ID AAB31889 standard; protein; 4393 AA.  
DE Amino acid sequence of a human protein.  
PN WO200105422-A2.  
PD 25-JAN-2001.  
PA (INMR) BIOMERIEUX STELHYS.  
Query Match 12.7%; Score 230; DB 4; Length 4393;  
Best Local Similarity 26.0%; Pred. No. 1.2e-09;  
RESULT 855  
ID ADL35758 standard; protein; 4393 AA.  
DE Human perlecan (heparan sulphate proteoglycan 2; HSPG2) protein.  
PN WO2004019893-A2.  
PD 11-MAR-2004.  
PA (RIGE-) RIGEL PHARM INC.  
Query Match 12.7%; Score 230; DB 8; Length 4393;  
Best Local Similarity 26.0%; Pred. No. 1.2e-09;  
RESULT 856  
ID ADQ39442 standard; protein; 4393 AA.

DE Human myocardial infarction-associated gene derived protein, SEQ ID 1105.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.7%; Score 230; DB 8; Length 4393;  
Best Local Similarity 26.0%; Pred. No. 1.2e-09;  
RESULT 857  
ID ABG23265 standard; protein; 4436 AA.  
DE Novel human diagnostic protein #23256.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.7%; Score 230; DB 4; Length 4436;  
Best Local Similarity 26.0%; Pred. No. 1.2e-09;  
RESULT 858  
ID ADL16585 standard; protein; 849 AA.  
DE Human 282p1g3 polypeptide #35.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 849;  
Best Local Similarity 25.6%; Pred. No. 1.4e-10;  
RESULT 859  
ID ADL16586 standard; protein; 851 AA.  
DE Human 282p1g3 polypeptide #36.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 851;  
Best Local Similarity 25.6%; Pred. No. 1.4e-10;  
RESULT 860  
ID AAW26506 standard; protein; 869 AA.  
DE Human Dmk receptor.  
PN US5656473-A.  
PD 12-AUG-1997.  
PA (REG-) REGENERON PHARM INC.  
Query Match 12.7%; Score 229.5; DB 2; Length 869;  
Best Local Similarity 26.4%; Pred. No. 1.5e-10;  
RESULT 861  
ID AAW26611 standard; protein; 869 AA.  
DE Human muscle-specific kinase (MUSK).  
PN WO9721811-A2.  
PD 19-JUN-1997.  
PA (REG-) REGENERON PHARM INC.  
Query Match 12.7%; Score 229.5; DB 2; Length 869;  
Best Local Similarity 26.4%; Pred. No. 1.5e-10;  
RESULT 862  
ID ADQ89844 standard; protein; 869 AA.  
DE Antagonist of cell cycle progression polypeptide #137.  
PN WO2004063362-A2.  
PD 29-JUL-2004.  
PA (CYCL-) CYCLACEL LTD.  
Query Match 12.7%; Score 229.5; DB 8; Length 869;  
Best Local Similarity 26.4%; Pred. No. 1.5e-10;  
RESULT 863  
ID ADL16446 standard; protein; 893 AA.  
DE Human 282p1g3 polypeptide #12.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 893;  
Best Local Similarity 25.6%; Pred. No. 1.5e-10;  
RESULT 864  
ID ADL16584 standard; protein; 893 AA.  
DE Human 282p1g3 polypeptide #34.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 893;  
Best Local Similarity 25.6%; Pred. No. 1.5e-10;  
RESULT 865  
ID ADL16625 standard; protein; 893 AA.  
DE Human 282p1g3 polypeptide #57.  
PN WO2004016734-A2.

PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 893;  
Best Local Similarity 25.6%; Pred. No. 1.5e-10;  
RESULT 866  
ID ADL16431 standard; protein; 893 AA.  
DE Human 282p1g3 polypeptide #3.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 893;  
Best Local Similarity 25.6%; Pred. No. 1.5e-10;  
RESULT 867  
ID ADL16626 standard; protein; 1117 AA.  
DE Human 282p1g3 polypeptide #58.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1117;  
Best Local Similarity 25.6%; Pred. No. 2.1e-10;  
RESULT 868  
ID ADL16590 standard; protein; 1117 AA.  
DE Human 282p1g3 polypeptide #37.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1117;  
Best Local Similarity 25.6%; Pred. No. 2.1e-10;  
RESULT 869  
ID ADL16447 standard; protein; 1117 AA.  
DE Human 282p1g3 polypeptide #13.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1117;  
Best Local Similarity 25.6%; Pred. No. 2.1e-10;  
RESULT 870  
ID ADL16433 standard; protein; 1117 AA.  
DE Human 282p1g3 polypeptide #4.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1117;  
Best Local Similarity 25.6%; Pred. No. 2.1e-10;  
RESULT 871  
ID ADL16592 standard; protein; 1117 AA.  
DE Human 282p1g3 polypeptide #39.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1117;  
Best Local Similarity 25.6%; Pred. No. 2.1e-10;  
RESULT 872  
ID AEM83685 standard; protein; 1171 AA.  
DE Human diagnostic and therapeutic pproteins SEQ ID NO.3934.  
PN WO2004023973-A2.  
PD 25-MAR-2004.  
PA (INCY-) INCYTE CORP.  
Query Match 12.7%; Score 229.5; DB 8; Length 1171;  
Best Local Similarity 25.6%; Pred. No. 2.2e-10;  
RESULT 873  
ID ADL16604 standard; protein; 1183 AA.  
DE Human 282p1g3 polypeptide #45.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1183;  
Best Local Similarity 25.6%; Pred. No. 2.3e-10;  
RESULT 874  
ID ADL16628 standard; protein; 1183 AA.  
DE Human 282p1g3 polypeptide #60.  
PN WO2004016734-A2.

PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1183;  
Query Match 25.6%; Pred. No. 2.3e-10;  
Best Local Similarity 25.6%; Pred. No. 2.3e-10;  
RESULT 875  
ID ADL16449 standard; protein; 1183 AA.  
DE Human 282PIG3 polypeptide #15.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1183;  
Query Match 25.6%; Pred. No. 2.3e-10;  
Best Local Similarity 25.6%; Pred. No. 2.3e-10;  
RESULT 876  
ID ADL16602 standard; protein; 1183 AA.  
DE Human 282PIG3 polypeptide #43.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1183;  
Query Match 25.6%; Pred. No. 2.3e-10;  
Best Local Similarity 25.6%; Pred. No. 2.3e-10;  
RESULT 877  
ID ADL16437 standard; protein; 1183 AA.  
DE Human 282PIG3 polypeptide #6.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1183;  
Query Match 25.6%; Pred. No. 2.3e-10;  
Best Local Similarity 25.6%; Pred. No. 2.3e-10;  
RESULT 878  
ID ADL16448 standard; protein; 1208 AA.  
DE Human 282PIG3 polypeptide #14.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1208;  
Query Match 25.6%; Pred. No. 2.3e-10;  
Best Local Similarity 25.6%; Pred. No. 2.3e-10;  
RESULT 879  
ID ADL16596 standard; protein; 1208 AA.  
DE Human 282PIG3 polypeptide #40.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1208;  
Query Match 25.6%; Pred. No. 2.3e-10;  
Best Local Similarity 25.6%; Pred. No. 2.3e-10;  
RESULT 880  
ID ADL16435 standard; protein; 1208 AA.  
DE Human 282PIG3 polypeptide #5.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1208;  
Query Match 25.6%; Pred. No. 2.3e-10;  
Best Local Similarity 25.6%; Pred. No. 2.3e-10;  
RESULT 881  
ID ADL16627 standard; protein; 1208 AA.  
DE Human 282PIG3 polypeptide #59.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1208;  
Query Match 25.6%; Pred. No. 2.3e-10;  
Best Local Similarity 25.6%; Pred. No. 2.3e-10;  
RESULT 882  
ID ADL16598 standard; protein; 1208 AA.  
DE Human 282PIG3 polypeptide #42.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1208;  
Query Match 25.6%; Pred. No. 2.3e-10;  
Best Local Similarity 25.6%; Pred. No. 2.3e-10;  
RESULT 883  
ID ADJ69602 standard; protein; 1224 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1408.  
PN WO2003087768-A2.  
PD 23-OCT-2003.

PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES. 12.7%; Score 229.5; DB 7; Length 1224;  
Query Match 25.6%; Pred. No. 2.4e-10;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 884  
ID ADL16443 standard; protein; 1224 AA.  
DE Human 282PIG3 polypeptide #9.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1224;  
Query Match 25.6%; Pred. No. 2.4e-10;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 885  
ID ADL16597 standard; protein; 1224 AA.  
DE Human 282PIG3 polypeptide #41.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1224;  
Query Match 25.6%; Pred. No. 2.4e-10;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 886  
ID ADL16621 standard; protein; 1224 AA.  
DE Human 282PIG3 polypeptide #53.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1224;  
Query Match 25.6%; Pred. No. 2.4e-10;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 887  
ID ADL16452 standard; protein; 1224 AA.  
DE Human 282PIG3 polypeptide #18.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1224;  
Query Match 25.6%; Pred. No. 2.4e-10;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 888  
ID ADL16623 standard; protein; 1224 AA.  
DE Human 282PIG3 polypeptide #55.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1224;  
Query Match 25.6%; Pred. No. 2.4e-10;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 889  
ID ADL16427 standard; protein; 1224 AA.  
DE Human 282PIG3 polypeptide #1.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1224;  
Query Match 25.6%; Pred. No. 2.4e-10;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 890  
ID ADL16455 standard; protein; 1224 AA.  
DE Human 282PIG3 polypeptide #21.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGESYS INC. 12.7%; Score 229.5; DB 8; Length 1224;  
Query Match 25.6%; Pred. No. 2.4e-10;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 891  
ID ADL16457 standard; protein; 1224 AA.  
DE Human 282PIG3 polypeptide #23.  
PN WO2004016734-A2.  
PD 26-FEB-2004.

PA (AGEN-) AGENSYS INC. 12.7%; Score 229.5; DB 8; Length 1224;  
Query Match 12.7%; Score 229.5; DB 8; Length 1224;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 893  
ID ADL16591 standard; protein; 1224 AA.  
DE Human 282P1G3 polypeptide #38.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1224;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 894  
ID ADL16620 standard; protein; 1224 AA.  
DE Human 282P1G3 polypeptide #52.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1224;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 895  
ID ADL16456 standard; protein; 1224 AA.  
DE Human 282P1G3 polypeptide #22.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1224;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 896  
ID ADL16615 standard; protein; 1224 AA.  
DE Human 282P1G3 polypeptide #50.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1224;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 897  
ID ADL16622 standard; protein; 1224 AA.  
DE Human 282P1G3 polypeptide #54.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1224;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 898  
ID ADL16444 standard; protein; 1224 AA.  
DE Human 282P1G3 polypeptide #10.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1224;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 899  
ID ADL16458 standard; protein; 1224 AA.  
DE Human 282P1G3 polypeptide #24.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1224;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 900  
ID ADL16550 standard; protein; 1224 AA.  
DE Human 282P1G3 polypeptide #27.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1224;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 901  
ID ADL16459 standard; protein; 1224 AA.  
DE Human 282P1G3 polypeptide #25.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.

Query Match 12.7%; Score 229.5; DB 8; Length 1224;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 902  
ID ADL16603 standard; protein; 1224 AA.  
DE Human 282P1G3 polypeptide #44.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1224;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 903  
ID ADL16453 standard; protein; 1224 AA.  
DE Human 282P1G3 polypeptide #19.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1224;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 904  
ID ADL16632 standard; protein; 1224 AA.  
DE Human 282P1G3 polypeptide #63.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1224;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 905  
ID ADL16609 standard; protein; 1224 AA.  
DE Human 282P1G3 polypeptide #47.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.7%; Score 229.5; DB 8; Length 1224;  
Best Local Similarity 25.6%; Pred. No. 2.4e-10;  
RESULT 906  
ID ADQ39441 standard; protein; 3588 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1104.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.7%; Score 229; DB 8; Length 3588;  
Best Local Similarity 26.0%; Pred. No. 1.1e-09;  
RESULT 907  
ID ADQ39440 standard; protein; 4346 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1103.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.7%; Score 229; DB 8; Length 4346;  
Best Local Similarity 26.0%; Pred. No. 1.5e-09;  
RESULT 908  
ID ADQ39439 standard; protein; 4347 AA.  
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1102.  
PN WO2004058052-A2.  
PD 15-JUL-2004.  
PA (APPL-) APPLERA CORP.  
Query Match 12.7%; Score 229; DB 8; Length 4347;  
Best Local Similarity 26.0%; Pred. No. 1.5e-09;  
RESULT 909  
ID ADJ69461 standard; protein; 4370 AA.  
DE Human heat mitochondrial protein as a therapeutic target SeqID1267.  
PN WO2003087768-A2.  
PD 23-OCT-2003.  
PA (MITO-) MITOKOR.  
PA (BUCK-) BUCK INST AGE RES.  
Query Match 12.7%; Score 229; DB 7; Length 4370;  
Best Local Similarity 26.0%; Pred. No. 1.5e-09;  
RESULT 910  
ID ABL6336 standard; protein; 1483 AA.  
DE Novel human diagnostic protein #16327.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.

Query Match 12.6%; Score 228; DB 4; Length 1483;  
Best Local Similarity 24.1%; Pred. No. 4.1e-10;  
RESULT 911  
ID AAD23360 standard; protein; 6642 AA.  
DE Bacterial polypeptide #5013.  
PN US2003233675-A1.  
PD 18-DEC-2003.  
PA (CAOY/) CAO Y.  
PA (HINK/) HINKLE G J.  
PA (SLAT/) SLATER S C.  
PA (CHEN/) CHEN X.  
PA (GOLD/) GOLDMAN B S.  
Query Match 12.5%; Score 226; DB 8; Length 6642;  
Best Local Similarity 23.7%; Pred. No. 4.8e-09;  
RESULT 912  
ID AAR92718 standard; protein; 478 AA.  
DE Mouse muscle-localized protein-tyrosine-kinase receptor 5' fragment.  
PN WO9602644-A1.  
PD 01-FEB-1996.  
PA (GEMY ) GENETICS INST INC.  
Query Match 12.5%; Score 225.5; DB 2; Length 478;  
Best Local Similarity 24.8%; Pred. No. 1.4e-10;  
RESULT 913  
ID AAR92716 standard; protein; 860 AA.  
DE Mouse muscle-localized protein-tyrosine-kinase receptor-1 isoform.  
PN WO9602644-A1.  
PD 01-FEB-1996.  
PA (GEMY ) GENETICS INST INC.  
Query Match 12.5%; Score 225.5; DB 2; Length 860;  
Best Local Similarity 24.8%; Pred. No. 3.2e-10;  
RESULT 914  
ID AAR92717 standard; protein; 868 AA.  
DE Mouse muscle-localized protein-tyrosine-kinase receptor-2 isoform.  
PN WO9602644-A1.  
PD 01-FEB-1996.  
PA (GEMY ) GENETICS INST INC.  
Query Match 12.5%; Score 225.5; DB 2; Length 868;  
Best Local Similarity 24.8%; Pred. No. 3.3e-10;  
RESULT 915  
ID AB010922 standard; protein; 869 AA.  
DE Human secreted protein (SECP) #18.  
PN WO200270669-A2.  
PD 12-SEP-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 12.5%; Score 225.5; DB 5; Length 869;  
Best Local Similarity 25.5%; Pred. No. 3.3e-10;  
RESULT 916  
ID AAE34390 standard; protein; 4391 AA.  
DE Human perlecan protein.  
PN WO200295415-A2.  
PD 28-NOV-2002.  
PA (OSTE-) OSTEOETER BIO TECH AS.  
Query Match 12.5%; Score 225; DB 6; Length 4391;  
Best Local Similarity 25.7%; Pred. No. 3.3e-09;  
RESULT 917  
ID ABG74129 standard; protein; 537 AA.  
DE Human hMUSK-R deletion mutant mMUSK-RI.  
PN US2002150876-A1.  
PD 17-OCT-2002.  
PA (PIPP/) PIPPIG S D.  
PA (VERE/) VERES G.  
Query Match 12.4%; Score 224.5; DB 4; Length 537;  
Best Local Similarity 26.0%; Pred. No. 2.1e-10;  
RESULT 918  
ID AAG77857 standard; protein; 537 AA.  
DE Mutant protein mMUSK-RI.  
PN WO200172834-A1.  
PD 04-OCT-2001.  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
Query Match 12.4%; Score 224.5; DB 4; Length 537;  
Best Local Similarity 26.0%; Pred. No. 2.1e-10;  
RESULT 919

ID ABG74130 standard; protein; 576 AA.  
DE Human hMUSK-R deletion mutant mMUSK-RII.  
PN US2002150876-A1.  
PD 17-OCT-2002.  
PA (PIPP/) PIPPIG S D.  
PA (VERE/) VERES G.  
Query Match 12.4%; Score 224.5; DB 4; Length 576;  
Best Local Similarity 26.0%; Pred. No. 2.3e-10;  
RESULT 920  
ID AAG77858 standard; protein; 576 AA.  
DE Mutant protein mMUSK-RII.  
PN WO200172834-A1.  
PD 04-OCT-2001.  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
Query Match 12.4%; Score 224.5; DB 4; Length 576;  
Best Local Similarity 26.0%; Pred. No. 2.3e-10;  
RESULT 921  
ID ABG74128 standard; protein; 869 AA.  
DE Human muscle specific tyrosine kinase receptor, hMUSK-R.  
PN US2002150876-A1.  
PD 17-OCT-2002.  
PA (PIPP/) PIPPIG S D.  
PA (VERE/) VERES G.  
Query Match 12.4%; Score 224.5; DB 4; Length 869;  
Best Local Similarity 26.0%; Pred. No. 4e-10;  
RESULT 922  
ID AAB68421 standard; protein; 869 AA.  
DE Amino acid sequence of a human MUSK-R polypeptide.  
PN WO200136659-A2.  
PD 25-MAY-2001.  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
Query Match 12.4%; Score 224.5; DB 4; Length 869;  
Best Local Similarity 26.0%; Pred. No. 4e-10;  
RESULT 923  
ID AAG77856 standard; protein; 869 AA.  
DE Protein of muscle specific tyrosine kinase receptor (hMUSK-R).  
PN WO200172834-A1.  
PD 04-OCT-2001.  
PA (NOVS ) NOVARTIS AG.  
PA (NOVS ) NOVARTIS-ERFINDUNGEN VERW GES MBH.  
Query Match 12.4%; Score 224.5; DB 4; Length 869;  
Best Local Similarity 26.0%; Pred. No. 4e-10;  
RESULT 924  
ID ADS17276 standard; protein; 869 AA.  
DE Human muscle specific tyrosine kinase receptor (MUSK-R) protein fragment.  
PN US6790614-B1.  
PD 14-SEP-2004.  
PA (NOVS ) NOVARTIS AG.  
Query Match 12.4%; Score 224.5; DB 8; Length 869;  
Best Local Similarity 26.0%; Pred. No. 4e-10;  
RESULT 925  
ID ABG22633 standard; protein; 981 AA.  
DE Novel human diagnostic protein #22624.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.4%; Score 224.5; DB 4; Length 981;  
Best Local Similarity 23.9%; Pred. No. 4.7e-10;  
RESULT 926  
ID ADR08740 standard; protein; 1113 AA.  
DE Human protein useful for treating neurological disease Seq 2246.  
PN EP1447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 12.4%; Score 224.5; DB 8; Length 1113;  
Best Local Similarity 25.3%; Pred. No. 5.6e-10;  
RESULT 927  
ID ADL16578 standard; protein; 1171 AA.  
DE Human 282PIG3 polypeptide #31.  
PN WO2004016734-A2.  
PD 26-FEB-2004.

PA (AGEN-) AGENSYS INC.  
Query Match 12.4%; Score 224.5; DB 8; Length 1171;  
Best Local Similarity 25.3%; Pred. No. 6e-10;  
RESULT 928  
ID ADL16624 standard; protein; 1171 AA.  
DE Human 282p1g3 polypeptide #56.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.4%; Score 224.5; DB 8; Length 1171;  
Best Local Similarity 25.3%; Pred. No. 6e-10;  
RESULT 929  
ID ADL1580 standard; protein; 1171 AA.  
DE Human 282p1g3 polypeptide #33.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.4%; Score 224.5; DB 8; Length 1171;  
Best Local Similarity 25.3%; Pred. No. 6e-10;  
RESULT 930  
ID ADL16429 standard; protein; 1171 AA.  
DE Human 282p1g3 polypeptide #2.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.4%; Score 224.5; DB 8; Length 1171;  
Best Local Similarity 25.3%; Pred. No. 6e-10;  
RESULT 931  
ID ADL16445 standard; protein; 1171 AA.  
DE Human 282p1g3 polypeptide #11.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.4%; Score 224.5; DB 8; Length 1171;  
Best Local Similarity 25.3%; Pred. No. 6e-10;  
RESULT 932  
ID ADE55236 standard; protein; 1224 AA.  
DE Human Protein AAB60937, SEQ ID NO 1049.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
Query Match 12.4%; Score 224.5; DB 7; Length 1224;  
Best Local Similarity 25.3%; Pred. No. 6.4e-10;  
RESULT 933  
ID ADL15032 standard; protein; 1224 AA.  
DE Human neural cell adhesion molecule protein for cancer treatment.  
PN WO2003068268-A2.  
PD 21-AUG-2003.  
PA (BIOI-) BIOINVENT INT AB.  
Query Match 12.4%; Score 224.5; DB 7; Length 1224;  
Best Local Similarity 25.3%; Pred. No. 6.4e-10;  
RESULT 934  
ID ADJ75519 standard; protein; 1224 AA.  
DE Marker gene related amino acid sequence SEQ ID NO:771.  
PN EFL1394274-A2.  
PD 03-MAR-2004.  
PA (GENO-) GENOX RES INC.  
Query Match 12.4%; Score 224.5; DB 8; Length 1224;  
Best Local Similarity 25.3%; Pred. No. 6.4e-10;  
RESULT 935  
ID ADL16454 standard; protein; 1224 AA.  
DE Human 282p1g3 polypeptide #20.  
PN WO2004016734-A2.  
PD 26-FEB-2004.  
PA (AGEN-) AGENSYS INC.  
Query Match 12.4%; Score 224.5; DB 8; Length 1224;  
Best Local Similarity 25.3%; Pred. No. 6.4e-10;  
RESULT 936  
ID ADN04062 standard; protein; 1224 AA.  
DE Antiproliferative protein sequence #226.  
PN WO2004028479-A2.  
PD 08-APR-2004.

PA (GETH) GENENTECH INC.  
Query Match 12.4%; Score 224.5; DB 8; Length 1224;  
Best Local Similarity 25.3%; Pred. No. 6.4e-10;  
RESULT 937  
ID ADQ19766 standard; protein; 1224 AA.  
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2585.  
PN WO2004048938-A2.  
PD 10-JUN-2004.  
PA (PROT-) PROTEIN DESIGN LABS INC.  
Query Match 12.4%; Score 224.5; DB 8; Length 1224;  
Best Local Similarity 25.3%; Pred. No. 6.4e-10;  
RESULT 938  
ID ADR14776 standard; protein; 1224 AA.  
DE Amino acid sequence of human MAPKX orthologue #8.  
PN WO2004066948-A2.  
PD 12-AUG-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match 12.4%; Score 224.5; DB 8; Length 1224;  
Best Local Similarity 25.3%; Pred. No. 6.4e-10;  
RESULT 939  
ID ADP29420 standard; protein; 1583 AA.  
DE Human secreted protein SEQ ID #187.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.4%; Score 224.5; DB 8; Length 1583;  
Best Local Similarity 23.9%; Pred. No. 9.1e-10;  
RESULT 940  
ID ADP29354 standard; protein; 1583 AA.  
DE Human secreted protein SEQ ID #121.  
PN WO2004035732-A2.  
PD 29-APR-2004.  
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.  
Query Match 12.4%; Score 224.5; DB 8; Length 1583;  
Best Local Similarity 23.9%; Pred. No. 9.1e-10;  
RESULT 941  
ID ABG20008 standard; protein; 1645 AA.  
DE Novel human diagnostic protein #19999.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.4%; Score 224.5; DB 4; Length 1645;  
Best Local Similarity 23.9%; Pred. No. 9.5e-10;  
RESULT 942  
ID ABG22631 standard; protein; 1765 AA.  
DE Novel human diagnostic protein #22622.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.4%; Score 224.5; DB 4; Length 1765;  
Best Local Similarity 23.9%; Pred. No. 1.1e-09;  
RESULT 943  
ID ABG12017 standard; protein; 1944 AA.  
DE Novel human diagnostic protein #12008.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.4%; Score 224.5; DB 4; Length 1944;  
Best Local Similarity 23.9%; Pred. No. 1.2e-09;  
RESULT 944  
ID AAE30259 standard; peptide; 68 AA.  
DE Human LP289 protein immunoglobulin-like domain #1.  
PN WO200274906-A2.  
PD 26-SEP-2002.  
PA (ELIL) LILLY & CO ELI.  
Query Match 12.4%; Score 224; DB 6; Length 68;  
Best Local Similarity 65.7%; Pred. No. 1.4e-11;  
RESULT 945  
ID ABG02117 standard; protein; 434 AA.  
DE Novel human diagnostic protein #2108.  
PN WO200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.

Query Match 12.4%; Score 224; DB 4; Length 434;  
Best Local Similarity 25.5%; Pred. No. 1.7e-10;  
RESULT 946  
ID AAW93829 standard; protein; 697 AA.  
DE Human polypeptide, SEQ ID NO: 3893.  
PN EPI130094-A2.  
PD 05-SEP-2001.  
PA (HELI-) HELIX RES INST.  
Query Match 12.4%; Score 224; DB 4; Length 697;  
Best Local Similarity 23.9%; Pred. No. 3.3e-10;  
RESULT 947  
ID ADL31860 standard; protein; 697 AA.  
DE Human protein encoded by a full length cDNA clone SeqID 3893.  
PN EPI1396543-A2.  
PD 10-MAR-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 12.4%; Score 224; DB 8; Length 697;  
Best Local Similarity 23.9%; Pred. No. 3.3e-10;  
RESULT 948  
ID ABG02019 standard; protein; 737 AA.  
DE Novel human diagnostic protein #2010.  
PN W0200175067-A2.  
PD 11-OCT-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.4%; Score 224; DB 4; Length 737;  
Best Local Similarity 25.5%; Pred. No. 3.5e-10;  
RESULT 949  
ID AAY08095 standard; protein; 1059 AA.  
DE Human PRO335 protein.  
PN W09914241-A2.  
PD 25-MAR-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 2; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 950  
ID AAY13393 standard; protein; 1059 AA.  
DE Amino acid sequence of protein PRO335.  
PN W09914328-A2.  
PD 25-MAR-1999.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 2; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 951  
ID AAY70672 standard; protein; 1059 AA.  
DE Human PRO335 protein.  
PN W0200015797-A2.  
PD 23-MAR-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 3; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 952  
ID ADC78602 standard; protein; 1059 AA.  
DE Human PRO335 protein.  
PN W0200015796-A2.  
PD 23-MAR-2000.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 3; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 953  
ID AAB80261 standard; protein; 1059 AA.  
DE Human PRO335 protein.  
PN W0200104311-A1.  
PD 18-JAN-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 4; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 954  
ID AAU00825 standard; protein; 1059 AA.  
DE Human immune response protein PRO335 (UNQ287).  
PN W0200119991-A1.  
PD 22-MAR-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 4; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 955  
ID ABU71639 standard; protein; 1059 AA.  
DE Human PRO polypeptide #50.  
PN US2002146709-A1.  
PD 10-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 956  
ID ABU71494 standard; protein; 1059 AA.  
DE Human PRO polypeptide #50.  
PN US2002192659-A1.  
PD 19-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 957  
ID ABU71940 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein PRO335.  
PN US2003003530-A1.  
PD 02-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 958  
ID ABO01823 standard; protein; 1059 AA.  
DE Novel human secreted and transmembrane protein PRO335.  
PN US2002197671-A1.  
PD 26-DEC-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 959  
ID ABU54396 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein PRO335.  
PN US2002132240-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 960  
ID ABO47411 standard; protein; 1059 AA.  
DE Human secreted/transmembrane polypeptide PRO335.  
PN US2003044839-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 961  
ID ABU64548 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #52.  
PN US2002160374-A1.  
PD 31-OCT-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 962  
ID ABU67394 standard; protein; 1059 AA.  
DE Human secreted protein PRO335.  
PN US2003023054-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 963  
ID ABO14914 standard; protein; 1059 AA.  
DE Human secreted / transmembrane polypeptide PRO335.  
PN US2003036060-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 964  
ID AAU00825 standard; protein; 1059 AA.  
DE Human immune response protein PRO335 (UNQ287).  
PN W0200119991-A1.  
PD 22-MAR-2001.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;



RESULT 964	ID ADAl6750 standard; protein; 1059 AA.	Query Match	12.4%;	Score 224;	DB 6;	Length 1059;
ID	ADU69671 standard; protein; 1059 AA.	Best Local Similarity	23.9%;	Pred. No. 5.8e-10;		
DE	Novel human secreted and transmembrane protein PRO335.					
PN	US2003017463-A1.					
PD	23-JAN-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	12.4%;	Score 224;	DB 6;	Length 1059;		
Best Local Similarity	23.9%;	Pred. No. 5.8e-10;				
RESULT 965	ID ADAl4853 standard; protein; 1059 AA.	Query Match	12.4%;	Score 224;	DB 6;	Length 1059;
ID	ADU14853 standard; protein; 1059 AA.	Best Local Similarity	23.9%;	Pred. No. 5.8e-10;		
DE	Human secreted / transmembrane polypeptide PRO335.					
PN	US2003027143-A1.					
PD	06-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	12.4%;	Score 224;	DB 6;	Length 1059;		
Best Local Similarity	23.9%;	Pred. No. 5.8e-10;				
RESULT 966	ID ADB29495 standard; protein; 1059 AA.	Query Match	12.4%;	Score 224;	DB 6;	Length 1059;
ID	ADB29495 standard; protein; 1059 AA.	Best Local Similarity	23.9%;	Pred. No. 5.8e-10;		
DE	Human secreted/transmembrane protein, #54.					
PN	US2003092002-A1.					
PD	15-MAY-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	12.4%;	Score 224;	DB 6;	Length 1059;		
Best Local Similarity	23.9%;	Pred. No. 5.8e-10;				
RESULT 967	ID ADA18351 standard; protein; 1059 AA.	Query Match	12.4%;	Score 224;	DB 6;	Length 1059;
ID	ADA18351 standard; protein; 1059 AA.	Best Local Similarity	23.9%;	Pred. No. 5.8e-10;		
DE	Human secreted/transmembrane protein, #54.					
PN	US2003039971-A1.					
PD	27-FEB-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	12.4%;	Score 224;	DB 6;	Length 1059;		
Best Local Similarity	23.9%;	Pred. No. 5.8e-10;				
RESULT 968	ID ABO32805 standard; protein; 1059 AA.	Query Match	12.4%;	Score 224;	DB 6;	Length 1059;
ID	ABO32805 standard; protein; 1059 AA.	Best Local Similarity	23.9%;	Pred. No. 5.8e-10;		
DE	Human secreted/transmembrane protein PRO335.					
PN	US2003045693-A1.					
PD	06-MAR-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	12.4%;	Score 224;	DB 6;	Length 1059;		
Best Local Similarity	23.9%;	Pred. No. 5.8e-10;				
RESULT 969	ID ABO34865 standard; protein; 1059 AA.	Query Match	12.4%;	Score 224;	DB 6;	Length 1059;
ID	ABO34865 standard; protein; 1059 AA.	Best Local Similarity	23.9%;	Pred. No. 5.8e-10;		
DE	Human PRO polypeptide #50.					
PN	US2003044793-A1.					
PD	06-MAR-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	12.4%;	Score 224;	DB 6;	Length 1059;		
Best Local Similarity	23.9%;	Pred. No. 5.8e-10;				
RESULT 970	ID ADA16326 standard; protein; 1059 AA.	Query Match	12.4%;	Score 224;	DB 6;	Length 1059;
ID	ADA16326 standard; protein; 1059 AA.	Best Local Similarity	23.9%;	Pred. No. 5.8e-10;		
DE	Human secreted/transmembrane protein, #54.					
PN	US2003049621-A1.					
PD	13-MAR-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	12.4%;	Score 224;	DB 6;	Length 1059;		
Best Local Similarity	23.9%;	Pred. No. 5.8e-10;				
RESULT 971	ID ADA42471 standard; protein; 1059 AA.	Query Match	12.4%;	Score 224;	DB 6;	Length 1059;
ID	ADA42471 standard; protein; 1059 AA.	Best Local Similarity	23.9%;	Pred. No. 5.8e-10;		
DE	Human secreted/transmembrane protein, #54.					
PN	US2003054401-A1.					
PD	20-MAR-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	12.4%;	Score 224;	DB 6;	Length 1059;		
Best Local Similarity	23.9%;	Pred. No. 5.8e-10;				
RESULT 972	ID ABO17543 standard; protein; 1059 AA.	Query Match	12.4%;	Score 224;	DB 6;	Length 1059;
ID	ABO17543 standard; protein; 1059 AA.	Best Local Similarity	23.9%;	Pred. No. 5.8e-10;		
DE	Human secreted/transmembrane protein, #54.					
PN	US2003064367-A1.					
PD	03-APR-2003.					
PA	(GETH ) GENENTECH INC.					
Query Match	12.4%;	Score 224;	DB 6;	Length 1059;		
Best Local Similarity	23.9%;	Pred. No. 5.8e-10;				
RESULT 973	ID ABO17543 standard; protein; 1059 AA.	Query Match				

DE Human secreted/transmembrane protein, #54.  
PN US2003059828-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 983  
ID ADC40312 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003059829-A1.  
PD 27-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 984  
ID ADC19136 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003036061-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 985  
ID ADC34436 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003036094-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 986  
ID ADC29491 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003049676-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 987  
ID ADC29022 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003049677-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 988  
ID ADC40907 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003054400-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 989  
ID ADC19564 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003054441-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 990  
ID ADC34012 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003073077-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 991  
ID ADC13082 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.

PN US2003073079-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 992  
ID ADC12534 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 993  
ID ADD05089 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 994  
ID ADD04095 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 995  
ID ADD03671 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003108983-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 996  
ID ADE34923 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003077583-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 997  
ID ADH59406 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003039972-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 998  
ID ADI38185 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 999  
ID ADJ26453 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1000  
ID ADE79368 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003135025-A1.



PD 14-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1017  
ID ADI65492 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003148419-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1018  
ID ADI37751 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003096340-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1019  
ID ADH97551 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003190610-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1020  
ID ADI65919 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003148371-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1021  
ID ADH60662 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2004023331-A1.  
PD 05-FEB-2004.  
PA (DESN ) DESNOYERS L.  
PA (GODD ) GODDARD A.  
PA (GODO ) GODOWSKI P J.  
PA (GURN ) GURNEY A L.  
PA (MATH ) MATHER J P.  
PA (WILL ) WILLIAMS P M.  
PA (WOOD ) WOOD W I.  
Query Match 12.4%; Score 224; DB 8; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1022  
ID ADJ99719 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003187238-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1023  
ID ADL08912 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003186358-A1.  
PD 02-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1024  
ID ADM25253 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003096233-A1.  
PD 22-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1025  
ID ADM30003 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003190611-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1026  
ID ADO06325 standard; protein; 1059 AA.  
DE Human PRO polypeptide #50.  
PN US6686451-B1.  
PD 03-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1027  
ID ADR11177 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2004137561-A1.  
PD 15-JUL-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1028  
ID ADR18086 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2004147017-A1.  
PD 29-JUL-2004.  
PA (ASHK ) ASHKENAZI A.  
PA (BOTS ) BOTSTEIN D.  
PA (DESN ) DESNOYERS L.  
PA (EATO ) EATON D L.  
PA (FERR ) FERRARA N.  
PA (FILV ) FILVAROFF E.  
PA (FONG ) FONG S.  
PA (GAOW ) GAO W.  
PA (GERB ) GERBER H.  
PA (GERR ) GERRITSEN M E.  
PA (GODD ) GODDARD A.  
PA (GODO ) GODOWSKI P J.  
PA (GRIM ) GRIMALDI C J.  
PA (GURN ) GURNEY A L.  
PA (HILL ) HILLAN K J.  
PA (KLJA ) KLAJAVIN I J.  
PA (MATH ) MATHER J P.  
PA (PANJ ) PAN J.  
PA (PAON ) PAONI N F.  
PA (ROYM ) ROY M A.  
PA (STEW ) STEWART T A.  
PA (TUMA ) TUMAS D.  
PA (WILL ) WILLIAMS P M.  
PA (WOOD ) WOOD W I.  
Query Match 12.4%; Score 224; DB 8; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1029  
ID AUT03762 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein, #54.  
PN US2003152922-A1.  
PD 14-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1059;  
Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
RESULT 1030  
ID ADS74725 standard; protein; 1059 AA.  
DE Human secreted/transmembrane protein #54.  
PN US2004185531-A1.  
PD 23-SEP-2004.  
PA (ASHK ) ASHKENAZI A.  
PA (BOTS ) BOTSTEIN D.  
PA (DESN ) DESNOYERS L.  
PA (EATO ) EATON D L.

PA (FERR/) FERRARA N. 12.4%; Score 224; DB 8; Length 1059;  
 PA (FILV/) FILVAROFF E. 23.9%; Pred. No. 5.8e-10;  
 PA (FONG/) GAO W. 12.4%; Score 224; DB 4; Length 1119;  
 PA (GERB/) GERBER H. 23.9%; Pred. No. 6.2e-10;  
 PA (GERR/) GERRITSEN M E. 12.4%; Score 224; DB 6; Length 1119;  
 PA (GODD/) GODDARD A. 23.9%; Pred. No. 6.2e-10;  
 PA (GODO/) GODOWSKI P J. 12.4%; Score 224; DB 6; Length 1119;  
 PA (GRIM/) GRIMALDI C J. 23.9%; Pred. No. 6.2e-10;  
 PA (GURN/) GURNEY A L. 12.4%; Score 224; DB 6; Length 1119;  
 PA (HILL/) HILLAN K J. 23.9%; Pred. No. 6.2e-10;  
 PA (KLJA/) KLJAVIN I J. 12.4%; Score 224; DB 6; Length 1119;  
 PA (MATH/) MATHER J P. 23.9%; Pred. No. 6.2e-10;  
 PA (PANJ/) PAN J. 12.4%; Score 224; DB 6; Length 1119;  
 PA (PAON/) PAONI N F. 23.9%; Pred. No. 6.2e-10;  
 PA (ROYM/) ROY M A. 12.4%; Score 224; DB 6; Length 1119;  
 PA (STEW/) STEWART T A. 23.9%; Pred. No. 6.2e-10;  
 PA (TUMA/) TUMAS D. 12.4%; Score 224; DB 6; Length 1119;  
 PA (WILL/) WILLIAMS P M. 23.9%; Pred. No. 6.2e-10;  
 PA (WOOD/) WOOD W I. 12.4%; Score 224; DB 6; Length 1119;  
 Query Match 12.4%; Score 224; DB 8; Length 1059;  
 Best Local Similarity 23.9%; Pred. No. 5.8e-10;  
 RESULT 1031  
 ID AAY08114 standard; protein; 1119 AA.  
 DE Human PRO326 protein.  
 PN WO9914241-A2.  
 PD 25-MAR-1999.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 2; Length 1119;  
 Query Match 12.4%; Score 224; DB 2; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1032  
 ID AAY70674 standard; protein; 1119 AA.  
 DE Human PRO326 protein.  
 PN WO200015797-A2.  
 PD 23-MAR-2000.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 3; Length 1119;  
 Query Match 12.4%; Score 224; DB 3; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1033  
 ID ADC78606 standard; protein; 1119 AA.  
 DE Human PRO326 protein.  
 PN WO200015796-A2.  
 PD 23-MAR-2000.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 3; Length 1119;  
 Query Match 12.4%; Score 224; DB 3; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1034  
 ID AAB80263 standard; protein; 1119 AA.  
 DE Human PRO326 protein.  
 PN WO200104311-A1.  
 PD 18-JAN-2001.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 4; Length 1119;  
 Query Match 12.4%; Score 224; DB 4; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1035  
 ID AAB48162 standard; protein; 1119 AA.  
 DE Human PRO326 polypeptide.  
 PN WO200075316-A1.  
 PD 14-DEC-2000.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 4; Length 1119;  
 Query Match 12.4%; Score 224; DB 4; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1036  
 ID AAU00827 standard; protein; 1119 AA.  
 DE Human immune response protein PRO326 (UNQ287).  
 PN WO200119991-A1.  
 PD 22-MAR-2001.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 4; Length 1119;  
 Query Match 12.4%; Score 224; DB 4; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1037  
 ID AAU12347 standard; protein; 1119 AA.  
 DE Human PRO326 polypeptide sequence.

PN WO20010466-A2.  
 PD 07-JUN-2001.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 4; Length 1119;  
 Query Match 12.4%; Score 224; DB 4; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1038  
 ID ABU71641 standard; protein; 1119 AA.  
 DE Human PRO polypeptide #52.  
 PN US2002146709-A1.  
 PD 10-OCT-2002.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 6; Length 1119;  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1039  
 ID ABO17791 standard; protein; 1119 AA.  
 DE Novel human secreted and transmembrane protein PRO326.  
 PN US2003032156-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 6; Length 1119;  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1040  
 ID ABU71496 standard; protein; 1119 AA.  
 DE Human PRO polypeptide #52.  
 PN US2002192659-A1.  
 PD 19-DEC-2002.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 6; Length 1119;  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1041  
 ID ABU81045 standard; protein; 1119 AA.  
 DE Human PRO polypeptide #176.  
 PN US2003004311-A1.  
 PD 02-JAN-2003.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 6; Length 1119;  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1042  
 ID ABU71942 standard; protein; 1119 AA.  
 DE Human secreted/transmembrane protein PRO326.  
 PN US2003003530-A1.  
 PD 02-JAN-2003.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 6; Length 1119;  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1043  
 ID ABO1825 standard; protein; 1119 AA.  
 DE Novel human secreted and transmembrane protein PRO326.  
 PN US2002197671-A1.  
 PD 26-DEC-2002.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 6; Length 1119;  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1044  
 ID ABU66745 standard; protein; 1119 AA.  
 DE Human PRO polypeptide #176.  
 PN US2003036180-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 6; Length 1119;  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1045  
 ID ABU54398 standard; protein; 1119 AA.  
 DE Human secreted/transmembrane protein PRO326.  
 PN US2002132240-A1.  
 PD 19-SEP-2002.  
 PA (GETH ) GENENTECH INC. 12.4%; Score 224; DB 6; Length 1119;  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1046  
 ID ABO47413 standard; protein; 1119 AA.  
 DE Human secreted/transmembrane polypeptide PRO326.  
 PN US2003044839-A1.

PD 06-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1047  
 ID ABUS9826 standard; protein; 1119 AA.  
 DE Novel secreted and transmembrane protein PRO326.  
 PN US2003017563-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1048  
 ID ABO25016 standard; protein; 1119 AA.  
 DE Human secreted/transmembrane protein (PRO) #176.  
 PN US2003036179-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1049  
 ID ABU64550 standard; protein; 1119 AA.  
 DE Human secreted/transmembrane protein, #54.  
 PN US2002160374-A1.  
 PD 31-OCT-2002.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1050  
 ID ABU67396 standard; protein; 1119 AA.  
 DE Human secreted protein PRO326.  
 PN US2003023054-A1.  
 PD 30-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1051  
 ID ABO14916 standard; protein; 1119 AA.  
 DE Human secreted / transmembrane polypeptide PRO326.  
 PN US2003036060-A1.  
 PD 20-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1052  
 ID ABU67021 standard; protein; 1119 AA.  
 DE Human secreted/transmembrane, PRO, protein SEQ ID 352.  
 PN US2003032155-A1.  
 PD 13-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1053  
 ID ABU69673 standard; protein; 1119 AA.  
 DE Novel human secreted and transmembrane protein PRO326.  
 PN US2003017463-A1.  
 PD 23-JAN-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1054  
 ID ABO14855 standard; protein; 1119 AA.  
 DE Human secreted / transmembrane polypeptide PRO326.  
 PN US200302143-A1.  
 PD 06-FEB-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1055  
 ID ADA45871 standard; protein; 1119 AA.  
 DE Novel human secreted and transmembrane protein PRO326.  
 PN US2003022328-A1.  
 PD 30-JAN-2003.

PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1056  
 ID ADA76302 standard; protein; 1119 AA.  
 DE Human PRO polypeptide #176.  
 PN US2003073212-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1057  
 ID ADB29499 standard; protein; 1119 AA.  
 DE Human secreted/transmembrane protein, #56.  
 PN US2003092002-A1.  
 PD 15-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1058  
 ID ADA18952 standard; protein; 1119 AA.  
 DE Human PRO polypeptide #176.  
 PN US2003054517-A1.  
 PD 20-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1059  
 ID ADA61575 standard; protein; 1119 AA.  
 DE Homo sapiens.  
 PN US2003049816-A1.  
 PD 13-MAR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1060  
 ID ADB19360 standard; protein; 1119 AA.  
 DE Novel human secreted and transmembrane protein PRO326.  
 PN US2003088796-A1.  
 PD 10-APR-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1061  
 ID ADB27901 standard; protein; 1119 AA.  
 DE Human PRO polypeptide #176.  
 PN US2003082704-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1062  
 ID ADA86380 standard; protein; 1119 AA.  
 DE Novel human secreted and transmembrane protein PRO326.  
 PN US2003082711-A1.  
 PD 01-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1063  
 ID ADB15944 standard; protein; 1119 AA.  
 DE Human PRO polypeptide #176.  
 PN US2003087350-A1.  
 PD 08-MAY-2003.  
 PA (GETH ) GENENTECH INC.  
 Query Match 12.4%; Score 224; DB 6; Length 1119;  
 Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
 RESULT 1064  
 ID ADA47730 standard; protein; 1119 AA.  
 DE Human PRO polypeptide #176.  
 PN US2003073215-A1.  
 PD 17-APR-2003.  
 PA (GETH ) GENENTECH INC.

Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1065  
ID ADA18355 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003039971-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1066  
ID ABO32807 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein PRO326.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1067  
ID ABO32808 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein PRO332.  
PN US2003045693-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1068  
ID ADA67525 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003068795-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1069  
ID ADB30532 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003068794-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1070  
ID ADA85828 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003082693-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1071  
ID ADA97040 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003082705-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1072  
ID ADA79344 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003082763-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1073  
ID ADA87483 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1074  
ID ADB16685 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003087349-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1075  
ID ABO34867 standard; protein; 1119 AA.  
DE Human PRO polypeptide #52.  
PN US2003044793-A1.  
PD 06-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1076  
ID ADA16330 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003049621-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1077  
ID ADA91777 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003082694-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1078  
ID ADB14840 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003087351-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1079  
ID ADB18801 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003073211-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1080  
ID ADA94016 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003077722-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1081  
ID ADB19912 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003082691-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1082  
ID ADB13224 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003082710-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1083  
ID ADA87483 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003087345-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;

ID	ADB29980 standard; protein;	1119 AA.
DE	Human PRO polypeptide #176.	
PN	US2003073214-A1.	
PD	17-APR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	12.4%; Score 224; DB 6;	Length 1119;
Best Local Similarity	23.9%; Pred. No. 6.2e-10;	
RESULT 1093		
ID	ADA80508 standard; protein;	1119 AA.
DE	Human PRO polypeptide #176.	
PN	US2003082761-A1.	
PD	01-MAY-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	12.4%; Score 224; DB 6;	Length 1119;
Best Local Similarity	23.9%; Pred. No. 6.2e-10;	
RESULT 1094		
ID	ADA75750 standard; protein;	1119 AA.
DE	Human PRO polypeptide #176.	
PN	US2003082703-A1.	
PD	01-MAY-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	12.4%; Score 224; DB 6;	Length 1119;
Best Local Similarity	23.9%; Pred. No. 6.2e-10;	
RESULT 1095		
ID	ADA46975 standard; protein;	1119 AA.
DE	Human PRO polypeptide #176.	
PN	US2003073210-A1.	
PD	17-APR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	12.4%; Score 224; DB 6;	Length 1119;
Best Local Similarity	23.9%; Pred. No. 6.2e-10;	
RESULT 1096		
ID	ADB25271 standard; protein;	1119 AA.
DE	Human PRO polypeptide SEQ ID NO 352.	
PN	US2003077721-A1.	
PD	24-APR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	12.4%; Score 224; DB 6;	Length 1119;
Best Local Similarity	23.9%; Pred. No. 6.2e-10;	
RESULT 1097		
ID	ADA93447 standard; protein;	1119 AA.
DE	Human PRO polypeptide #176.	
PN	US2003077721-A1.	
PD	24-APR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	12.4%; Score 224; DB 6;	Length 1119;
Best Local Similarity	23.9%; Pred. No. 6.2e-10;	
RESULT 1098		
ID	ADB26797 standard; protein;	1119 AA.
DE	Human PRO polypeptide #176.	
PN	US2003092147-A1.	
PD	15-MAY-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	12.4%; Score 224; DB 6;	Length 1119;
Best Local Similarity	23.9%; Pred. No. 6.2e-10;	
RESULT 1099		
ID	ADB31084 standard; protein;	1119 AA.
DE	Human PRO polypeptide #176.	
PN	US2003096386-A1.	
PD	22-MAY-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	12.4%; Score 224; DB 6;	Length 1119;
Best Local Similarity	23.9%; Pred. No. 6.2e-10;	
RESULT 1100		
ID	ADA61012 standard; protein;	1119 AA.
DE	Homo sapiens.	
PN	US2003049817-A1.	
PD	13-MAR-2003.	
PA	(GETH ) GENENTECH INC.	
Query Match	12.4%; Score 224; DB 6;	Length 1119;
Best Local Similarity	23.9%; Pred. No. 6.2e-10;	
RESULT 1101		
ID	ADB24159 standard; protein;	1119 AA.



DE Human PRO polypeptide SEQ ID NO 352.  
PN US2003077714-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1102  
ID ADA96488 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003082690-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1103  
ID ADA81060 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003082702-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1104  
ID ADA95936 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003082759-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1105  
ID ADB26245 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003082760-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1106  
ID ADB21730 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003082765-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 6; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1107  
ID ADA77509 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003068797-A1.  
PD 10-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1108  
ID ADB18249 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003077710-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1109  
ID ADA86932 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003082709-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1110  
ID ADA16754 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003059909-A1.

PN US2003039969-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1111  
ID ADA13183 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003049622-A1.  
PD 13-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1112  
ID ADA42051 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003082540-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1113  
ID ADA88035 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003082700-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1114  
ID ADA46423 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003054516-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1115  
ID ADA17398 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003017498-A1.  
PD 23-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1116  
ID ADA42901 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003054351-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1117  
ID ADB28453 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003082699-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1118  
ID ADB29005 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003082706-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1119  
ID ADA76957 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003059909-A1.

PD 27-MAR-2003.	PA (GETH ) GENENTECH INC.	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;
Best Local Similarity	23.9%;	Pred. No. 6.2e-10;				
RESULT 1120						
DE Human PRO polypeptide #176.						
PN US2003087352-A1.						
PD 08-MAY-2003.						
PA (GETH ) GENENTECH INC.						
Query Match	12.4%;	Score 224;	DB 7;	Length 1119;		
Best Local Similarity	23.9%;	Pred. No. 6.2e-10;				
RESULT 1130						
ID ADB38644 standard; protein; 1119 AA.						
DE Novel human secreted and transmembrane protein PRO326.						
PN US2003082766-A1.						
PD 01-MAY-2003.						
PA (GETH ) GENENTECH INC.						
Query Match	12.4%;	Score 224;	DB 7;	Length 1119;		
Best Local Similarity	23.9%;	Pred. No. 6.2e-10;				
RESULT 1131						
ID ADB38092 standard; protein; 1119 AA.						
DE Novel human secreted and transmembrane protein PRO326.						
PN US2003087347-A1.						
PD 08-MAY-2003.						
PA (GETH ) GENENTECH INC.						
Query Match	12.4%;	Score 224;	DB 7;	Length 1119;		
Best Local Similarity	23.9%;	Pred. No. 6.2e-10;				
RESULT 1132						
ID ADB66564 standard; protein; 1119 AA.						
DE Novel human secreted and transmembrane protein PRO326.						
PN US2003082689-A1.						
PD 01-MAY-2003.						
PA (GETH ) GENENTECH INC.						
Query Match	12.4%;	Score 224;	DB 7;	Length 1119;		
Best Local Similarity	23.9%;	Pred. No. 6.2e-10;				
RESULT 1133						
ID ADB89644 standard; protein; 1119 AA.						
DE Human PRO polypeptide #176.						
PN US2003082698-A1.						
PD 01-MAY-2003.						
PA (GETH ) GENENTECH INC.						
Query Match	12.4%;	Score 224;	DB 7;	Length 1119;		
Best Local Similarity	23.9%;	Pred. No. 6.2e-10;				
RESULT 1134						
ID ADB90376 standard; protein; 1119 AA.						
DE Human PRO polypeptide #176.						
PN US2003082762-A1.						
PD 01-MAY-2003.						
PA (GETH ) GENENTECH INC.						
Query Match	12.4%;	Score 224;	DB 7;	Length 1119;		
Best Local Similarity	23.9%;	Pred. No. 6.2e-10;				
RESULT 1135						
ID ADB77820 standard; protein; 1119 AA.						
DE Human secreted/transmembrane protein, #56.						
PN US2003077654-A1.						
PD 24-APR-2003.						
PA (GETH ) GENENTECH INC.						
Query Match	12.4%;	Score 224;	DB 7;	Length 1119;		
Best Local Similarity	23.9%;	Pred. No. 6.2e-10;				
RESULT 1136						
ID ADB39477 standard; protein; 1119 AA.						
DE Novel human secreted and transmembrane protein PRO326.						
PN US2003082764-A1.						
PD 01-MAY-2003.						
PA (GETH ) GENENTECH INC.						
Query Match	12.4%;	Score 224;	DB 7;	Length 1119;		
Best Local Similarity	23.9%;	Pred. No. 6.2e-10;				
RESULT 1137						
ID ADB74956 standard; protein; 1119 AA.						
DE Human secreted/transmembrane protein, #56.						
PN US2003082542-A1.						
PD 01-MAY-2003.						
PA (GETH ) GENENTECH INC.						
Query Match	12.4%;	Score 224;	DB 7;	Length 1119;		
Best Local Similarity	23.9%;	Pred. No. 6.2e-10;				
RESULT 1138						
ID ADA92329 standard; protein; 1119 AA.						
DE Novel human secreted and transmembrane protein PRO326.						
PN US2003082712-A1.						
PD 01-MAY-2003.						
PA (GETH ) GENENTECH INC.						
Query Match	12.4%;	Score 224;	DB 7;	Length 1119;		
Best Local Similarity	23.9%;	Pred. No. 6.2e-10;				
RESULT 1127				</		

```
RESULT 1138
ID ADB47100 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082687-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1139
ID ADB86707 standard; protein; 1119 AA.
DE Human PRO polypeptide #176.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1140
ID ADB77312 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082696-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1141
ID ADB34469 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077717-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1142
ID ADB35573 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077719-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1143
ID ADB33917 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077716-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1144
ID ADB35021 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077718-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1145
ID ADB36125 standard; protein; 1119 AA.
DE Human PRO polypeptide SEQ ID NO 352.
PN US2003077720-A1.
PD 24-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1146
ID ADB46520 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1147
ID ADB34016 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082697-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1148
ID ADB39802 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059828-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1149
ID ADB40316 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003059829-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1150
ID ADB19140 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003036061-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1151
ID ADB34440 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003036094-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1152
ID ADB29495 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049676-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1153
ID ADB23026 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003049677-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1154
ID ADB40911 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054400-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1155
ID ADB19568 standard; protein; 1119 AA.
DE Human secreted/transmembrane protein, #56.
PN US2003054441-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
RESULT 1156
ID ADB34016 standard; protein; 1119 AA.
DE Novel human secreted and transmembrane protein PRO326.
PN US2003082692-A1.
PD 01-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 12.4%; Score 224; DB 7; Length 1119;
Best Local Similarity 23.9%; Pred. No. 6.2e-10;
```

DE Human secreted/transmembrane protein, #56.  
PN US2003073077-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1157  
ID ADC13086 standard; protein; 1119 AA.  
DE Novel human secreted/transmembrane protein, #56.  
PN US2003073079-A1.  
PD 17-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1158  
ID ADC50393 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003092106-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1159  
ID ADC71940 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003092107-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1160  
ID ADC59919 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003092105-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1161  
ID ADC57280 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1162  
ID ADC57280 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003087366-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1163  
ID ADC60471 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003087367-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1164  
ID ADC50946 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003087361-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1165  
ID ADC65473 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003194770-A1.

PN US2003087362-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1166  
ID ADC54571 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein Seq ID352.  
PN US2003087363-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1167  
ID ADC53532 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein Seq ID352.  
PN US2003087364-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1168  
ID ADC59055 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein Seq ID352.  
PN US2003087359-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1169  
ID ADC55933 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein Seq ID352.  
PN US2003087360-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1170  
ID ADC58503 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein Seq ID352.  
PN US2003087346-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1171  
ID ADC12538 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003082541-A1.  
PD 01-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1172  
ID ADD03177 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003092104-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1173  
ID ADC90169 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003087348-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1174  
ID ADC69588 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003194770-A1.

PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1175  
ID ADC48477 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003194773-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1176  
ID ADD10006 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003194776-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1177  
ID ADD04581 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003087354-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1178  
ID ADC80537 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003092103-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1179  
ID ADD11044 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003194774-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1180  
ID ADC47925 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003194771-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1181  
ID ADD05093 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003104469-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1182  
ID ADC79985 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003087358-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1183  
ID ADD09454 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003194775-A1.  
PD 16-OCT-2003.

PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1184  
ID ADD04099 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003104381-A1.  
PD 05-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1185  
ID ADD03675 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003108983-A1.  
PD 12-JUN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1186  
ID ADD41167 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003203438-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1187  
ID ADD52306 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003194769-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1188  
ID ADD53046 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003194792-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1189  
ID ADD53598 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003203437-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1190  
ID ADD51754 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003194779-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1191  
ID ADD02553 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003203431-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1192  
ID ADD01987 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003203430-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.

Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1193  
ID ADP54169 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003203432-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1194  
ID ADP92486 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US200319030-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1195  
ID ADP91382 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US200319055-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1196  
ID ADE03596 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US200319057-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1197  
ID ADE32293 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003194765-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1198  
ID ADE22225 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US200319056-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1199  
ID ADD79449 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003203428-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1200  
ID ADE41985 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003194772-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1201  
ID ADE17802 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US200319023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1202  
ID ADP91934 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003199053-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1203  
ID ADE33397 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003194767-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1204  
ID ADE33949 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003194791-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1205  
ID ADD80001 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207417-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1206  
ID ADD93038 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003194768-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1207  
ID ADE19458 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003199025-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1208  
ID ADE34927 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003077583-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1209  
ID ADE18906 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003199026-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1210  
ID ADE43102 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003199033-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1211  
ID ADE17802 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003199023-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;

RESULT 1211	ID ADE92793 standard; protein; 1119 AA.	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;
	DE Human PRO polypeptide #176.	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;		
	PN US2003194777-A1.					
	PD 16-OCT-2003.					
	PA (GETH ) GENENTECH INC.					
	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;	
	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;			
RESULT 1212	ID ADG21502 standard; protein; 1119 AA.	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;
	DE Novel human secreted and transmembrane protein PRO326.	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;		
	PN US2003207355-A1.					
	PD 06-NOV-2003.					
	PA (GETH ) GENENTECH INC.					
	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;	
	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;			
RESULT 1222	ID ADG23143 standard; protein; 1119 AA.	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;
	DE Novel human secreted and transmembrane protein PRO326.	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;		
	PN US2003207384-A1.					
	PD 06-NOV-2003.					
	PA (GETH ) GENENTECH INC.					
	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;	
	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;			
RESULT 1223	ID ADF97478 standard; protein; 1119 AA.	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;
	DE Human PRO polypeptide #176.	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;		
	PN US2003207370-A1.					
	PD 06-NOV-2003.					
	PA (GETH ) GENENTECH INC.					
	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;	
	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;			
RESULT 1224	ID ADG80542 standard; protein; 1119 AA.	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;
	DE Human PRO polypeptide #176.	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;		
	PN US2003207373-A1.					
	PD 06-NOV-2003.					
	PA (GETH ) GENENTECH INC.					
	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;	
	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;			
RESULT 1225	ID ADG79990 standard; protein; 1119 AA.	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;
	DE Human PRO polypeptide #176.	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;		
	PN US2003207372-A1.					
	PD 06-NOV-2003.					
	PA (GETH ) GENENTECH INC.					
	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;	
	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;			
RESULT 1226	ID ADH59410 standard; protein; 1119 AA.	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;
	DE Human secreted/transmembrane protein, #56.	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;		
	PN US2003039972-A1.					
	PD 27-FEB-2003.					
	PA (GETH ) GENENTECH INC.					
	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;	
	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;			
RESULT 1227	ID ADH55282 standard; protein; 1119 AA.	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;
	DE Novel human secreted and transmembrane protein PRO326.	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;		
	PN US2003207381-A1.					
	PD 06-NOV-2003.					
	PA (GETH ) GENENTECH INC.					
	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;	
	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;			
RESULT 1228	ID ADH55834 standard; protein; 1119 AA.	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;
	DE Novel human secreted and transmembrane protein PRO326.	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;		
	PN US2003207379-A1.					
	PD 06-NOV-2003.					
	PA (GETH ) GENENTECH INC.					
	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;	
	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;			
RESULT 1229	ID ADI38189 standard; protein; 1119AA.	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;
	DE Human PRO polypeptide #176.	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;		
	PN US2003199034-A1.					
	PD 23-OCT-2003.					
	PA (GETH ) GENENTECH INC.					
	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;	
	Best Local Similarity	23.9%;	Pred. No. 6.2e-10;			
RESULT 1230	ID ADE04664 standard; protein; 1119 AA.	Query Match	12.4%;	Score 224;	DB 7;	Length 1119;
	DE Human PRO polypeptide #1					

DE Human secreted/transmembrane protein, #56.  
PN US2003054352-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1230  
ID ADI64053 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207385-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1231  
ID ADI65002 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207386-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1232  
ID ADI63501 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207387-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1233  
ID ADH81915 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207388-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1234  
ID ADH81363 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207377-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1235  
ID ADJ26457 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003054349-A1.  
PD 20-MAR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1236  
ID ADM82532 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003087355-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1237  
ID ADN15931 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003087353-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1238  
ID ADN16560 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003211571-A1.

PN US2003087385-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1239  
ID ADN15379 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003087356-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1240  
ID ADN14827 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003087357-A1.  
PD 08-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 7; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1241  
ID ADC81089 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003092115-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1242  
ID ADE79372 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003135025-A1.  
PD 17-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1243  
ID ADD76537 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003100087-A1.  
PD 29-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1244  
ID ADD87901 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003092113-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1245  
ID ADD86305 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003203440-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1246  
ID ADE79796 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003130489-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1247  
ID ADE75753 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003211571-A1.



PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1248  
ID ADE73472 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
FN US2003129592-A1.  
PD 10-JUL-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1249  
ID ADE23329 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
FN US2003092108-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1250  
ID ADE23881 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
FN US2003092110-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1251  
ID ADE24524 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
FN US2003092111-A1.  
PD 15-MAY-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1252  
ID ADE87349 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
FN US2003203439-A1.  
PD 30-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1253  
ID ADE89215 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
FN US2003199062-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1254  
ID ADE74007 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
FN US2003148370-A1.  
PD 07-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1255  
ID ADE18354 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
FN US2003194794-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1256  
ID ADE88663 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
FN US2003199054-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.

PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1257  
ID ADE99561 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
FN US2003211576-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1258  
ID ADE94683 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
FN US2003199027-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1259  
ID ADE91094 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
FN US2003199061-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1260  
ID ADE95235 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
FN US2003199052-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1261  
ID ADE93345 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
FN US2003199060-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1262  
ID ADF34926 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
FN US2003199029-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1263  
ID ADE98680 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
FN US2003211569-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1264  
ID ADE92241 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
FN US2003199051-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1265  
ID ADE90542 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
FN US2003199063-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.

Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1266  
ID ADE91689 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US200319058-A1.  
PD 23-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1267  
ID ADE99107 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003211568-A1.  
PD 13-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1268  
ID ADG40577 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003225253-A1.  
PD 04-DEC-2003.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GURN/) GURNEY A L.  
PA (MATH/) MATHER J P.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1269  
ID ADF73971 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003180312-A1.  
PD 25-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1270  
ID ADG02268 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207352-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1271  
ID ADG22054 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207360-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1272  
ID ADG20124 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207376-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1273  
ID ADF98030 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207422-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1274  
ID ADG08358 standard; protein; 1119 AA.

ID ADG24247 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207426-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1275  
ID ADF98601 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003208055-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1276  
ID ADG03432 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207351-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1277  
ID ADF99153 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207353-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1278  
ID ADG16738 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207359-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1279  
ID ADG05197 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207375-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1280  
ID ADG19464 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207425-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1281  
ID ADF73547 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003166051-A1.  
PD 04-SEP-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1282  
ID ADG13301 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207357-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1283  
ID ADG08358 standard; protein; 1119 AA.

DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207424-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1284  
ID ADG1528 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003219885-A1.  
PD 27-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1285  
ID ADF96926 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207371-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1286  
ID ADG06111 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207374-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1287  
ID AGD23695 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207389-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1288  
ID ADG03984 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207423-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1289  
ID ADG24885 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207427-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1290  
ID ADG07182 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207350-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1291  
ID ADG07734 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207356-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1292  
ID ADG55229 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.

PN US2003194778-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1293  
ID ADG60893 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207390-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1294  
ID ADG61997 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207428-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1295  
ID ADG92390 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003027145-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1296  
ID ADG82198 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207358-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1297  
ID ADG57437 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207362-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1298  
ID ADG56885 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207364-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1299  
ID ADG55781 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207365-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1300  
ID ADG58541 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207368-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1301  
ID ADG70907 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207420-A1.

PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1302  
ID ADG92817 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003027146-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1303  
ID ADG57989 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207363-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1304  
ID ADG53573 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207415-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1305  
ID ADG71459 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207421-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1306  
ID ADG81646 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003207805-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1307  
ID ADH30608 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003077723-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1308  
ID ADH11975 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207419-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1309  
ID ADG52397 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207414-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1310  
ID ADG54125 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207416-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.

Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1311  
ID ADG81094 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003194793-A1.  
PD 16-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1312  
ID ADG56333 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207366-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1313  
ID ADH12599 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207378-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1314  
ID ADG61445 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207429-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1315  
ID ADH28532 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003022331-A1.  
PD 30-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1316  
ID ADG54677 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207367-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1317  
ID ADG59717 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207369-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1318  
ID ADH20606 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2004005553-A1.  
PD 08-JAN-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1319  
ID ADH07461 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2004006211-A1.  
PD 08-JAN-2004.  
PA (DESN/) DESNOYERS L.  
PA (GODD/) GODDARD A.



Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1336  
ID ADJ63563 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2004039164-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1337  
ID ADJ30007 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003190611-A1.  
PD 09-OCT-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1338  
ID ADJ77458 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2004038336-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1339  
ID ADJ65580 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2004038335-A1.  
PD 26-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1340  
ID ADJ27716 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2004048333-A1.  
PD 11-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1341  
ID ADJ42440 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2004058424-A1.  
PD 25-MAR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1342  
ID ADO06329 standard; protein; 1119 AA.  
DE Human PRO polypeptide #52.  
PN US6686451-B1.  
PD 03-FEB-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1343  
ID ADM28302 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2004077064-A1.  
PD 22-APR-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1344  
ID ADR11181 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2004137561-A1.  
PD 15-JUL-2004.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1345  
ID ADR18090 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2004147017-A1.  
PD 29-JUL-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.  
PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KLJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1346  
ID ADI95784 standard; protein; 1119 AA.  
DE Human PRO polypeptide #176.  
PN US2003077659-A1.  
PD 24-APR-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1347  
ID ADI96336 standard; protein; 1119 AA.  
DE Novel human secreted and transmembrane protein PRO326.  
PN US2003207354-A1.  
PD 06-NOV-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1348  
ID ADT03766 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein, #56.  
PN US2003152922-A1.  
PD 14-AUG-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1349  
ID ADS74729 standard; protein; 1119 AA.  
DE Human secreted/transmembrane protein #56.  
PN US2004185531-A1.  
PD 23-SEP-2004.  
PA (ASHK/) ASHKENAZI A.  
PA (BOTS/) BOTSTEIN D.  
PA (DESN/) DESNOYERS L.  
PA (EATO/) EATON D L.  
PA (FERR/) FERRARA N.  
PA (FILV/) FILVAROFF E.  
PA (FONG/) FONG S.  
PA (GAOW/) GAO W.  
PA (GERB/) GERBER H.  
PA (GERR/) GERRITSEN M E.  
PA (GODD/) GODDARD A.  
PA (GODO/) GODOWSKI P J.  
PA (GRIM/) GRIMALDI C J.

PA (GURN/) GURNEY A L.  
PA (HILL/) HILLAN K J.  
PA (KLJA/) KJAVIN I J.  
PA (MATH/) MATHER J P.  
PA (PANJ/) PAN J.  
PA (PAON/) PAONI N F.  
PA (ROYM/) ROY M A.  
PA (STEW/) STEWART T A.  
PA (TUMA/) TUMAS D.  
PA (WILL/) WILLIAMS P M.  
PA (WOOD/) WOOD W I.  
Query Match 12.4%; Score 224; DB 8; Length 1119;  
Best Local Similarity 23.9%; Pred. No. 6.2e-10;  
RESULT 1350  
ID ADA55073 standard; protein; 1251 AA.  
DE Human protein, SEQ ID 2641.  
PN EPI293569-A2.  
PD 19-MAR-2003.  
PA (HELI-) HELIX RES INST.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 12.4%; Score 224; DB 6; Length 1251;  
Best Local Similarity 25.9%; Pred. No. 7.3e-10;  
RESULT 1351  
ID ABU11674 standard; protein; 380 AA.  
DE Human MDT polypeptide SEQ ID 621.  
PN WQ200279449-A2.  
PD 10-OCT-2002.  
PA (INCY-) INCYTE GENOMICS INC.  
Query Match 12.3%; Score 223; DB 6; Length 380;  
Best Local Similarity 26.4%; Pred. No. 1.7e-10;  
RESULT 1352  
ID AAY53028 standard; protein; 414 AA.  
DE Human secreted protein clone cw1000\_2 protein sequence SEQ ID NO:62.  
PN WQ9957132-A1.  
PD 11-NOV-1999.  
PA (GEMY) GENETICS INST INC.  
Query Match 12.3%; Score 223; DB 3; Length 414;  
Best Local Similarity 24.9%; Pred. No. 1.9e-10;  
RESULT 1353  
ID ABJ20228 standard; protein; 798 AA.  
DE Human IG gene related protein SEQ ID No 51.  
PN WQ200299040-A2.  
PD 12-DEC-2002.  
PA (EXEL-) EXELIXIS INC.  
Query Match 12.3%; Score 223; DB 6; Length 798;  
Best Local Similarity 24.8%; Pred. No. 4.8e-10;  
RESULT 1354  
ID ABB97578 standard; protein; 1179 AA.  
DE Novel human protein SEQ ID NO: 846.  
PN WQ20022860-A2.  
PD 21-MAR-2002.  
PA (HYSE-) HYSE INC.  
Query Match 12.3%; Score 223; DB 5; Length 1179;  
Best Local Similarity 24.8%; Pred. No. 8.2e-10;  
RESULT 1355  
ID ADR28014 standard; protein; 1179 AA.  
DE Long form IGSF9 protein.  
PN WQ2004066933-A2.  
PD 12-AUG-2004.  
PA (MCLA/) MCLACHLAN K.  
PA (GLAS/) GLASER S.  
PA (PEAC/) PEACH R J.  
PA (ROWE/) ROWE T.  
Query Match 12.3%; Score 223; DB 8; Length 1179;  
Best Local Similarity 24.8%; Pred. No. 8.2e-10;  
RESULT 1356  
ID ADR28013 standard; protein; 1179 AA.  
DE Long form full-length IGSF9 protein.  
PN WQ2004066933-A2.  
PD 12-AUG-2004.  
PA (MCLA/) MCLACHLAN K.  
PA (GLAS/) GLASER S.  
PA (PEAC/) PEACH R J.

PA (ROWE/) ROWE T.  
Query Match 12.3%; Score 223; DB 8; Length 1179;  
Best Local Similarity 24.8%; Pred. No. 8.2e-10;  
RESULT 1357  
ID ADR09753 standard; protein; 595 AA.  
DE Human protein useful for treating neurological disease Seq 3259.  
PN EPI447413-A2.  
PD 18-AUG-2004.  
PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
Query Match 12.3%; Score 222; DB 8; Length 595;  
Best Local Similarity 27.2%; Pred. No. 3.9e-10;  
RESULT 1358  
ID ABB10202 standard; protein; 744 AA.  
DE Human cDNA SEQ ID NO: 510.  
PN WQ200154474-A2.  
PD 02-AUG-2001.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.3%; Score 222; DB 4; Length 744;  
Best Local Similarity 23.6%; Pred. No. 5.3e-10;  
RESULT 1359  
ID ABP66789 standard; protein; 744 AA.  
DE Human polypeptide SEQ ID NO 510.  
PN US2002090672-A1.  
PD 11-JUL-2002.  
PA (ROSE/) ROSEN C A.  
PA (RUBE/) RUBEN S M.  
PA (BARA/) BARASH S C.  
Query Match 12.3%; Score 222; DB 5; Length 744;  
Best Local Similarity 23.6%; Pred. No. 5.3e-10;  
RESULT 1360  
ID ADH72194 standard; protein; 1068 AA.  
DE Human protein of the invention NOVsid SEQ ID NO:1090.  
PN WQ2003102155-A2.  
PD 11-DEC-2003.  
PA (CURA-) CURAGEN CORP.  
Query Match 12.3%; Score 222; DB 8; Length 1068;  
Best Local Similarity 24.2%; Pred. No. 8.7e-10;  
RESULT 1361  
ID AAW42087 standard; protein; 1571 AA.  
DE Human Down syndrome-cell adhesion molecule DS-CAM2.  
PN WQ9817795-A1.  
PD 30-APR-1998.  
PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
Query Match 12.2%; Score 221; DB 2; Length 1571;  
Best Local Similarity 28.6%; Pred. No. 1.8e-09;  
RESULT 1362  
ID AAW42086 standard; protein; 1910 AA.  
DE Human Down syndrome-cell adhesion molecule DS-CAM1.  
PN WQ9817795-A1.  
PD 30-APR-1998.  
PA (CEDA-) CEDARS SINAI MEDICAL CENT.  
Query Match 12.2%; Score 221; DB 2; Length 1910;  
Best Local Similarity 28.6%; Pred. No. 2.3e-09;  
RESULT 1363  
ID ADK71092 standard; protein; 2012 AA.  
DE Human MP21 polypeptide.  
PN WQ2004015073-A2.  
PD 19-FEB-2004.  
PA (EXEL-) EXELIXIS INC.  
Query Match 12.2%; Score 221; DB 8; Length 2012;  
Best Local Similarity 28.6%; Pred. No. 2.5e-09;  
RESULT 1364  
ID AAB25586 standard; protein; 364 AA.  
DE Protein encoded by human secreted protein gene #11.  
PN WQ200029435-A1.  
PD 25-MAY-2000.  
PA (HUMA-) HUMAN GENOME SCI INC.  
Query Match 12.2%; Score 220.5; DB 3; Length 364;  
Best Local Similarity 26.0%; Pred. No. 2.7e-10;  
RESULT 1365  
ID ADA27058 standard; protein; 364 AA.  
DE Human novel secreted protein from cDNA HOUDJ81 #1.  
PN US2003055231-A1.

PD 20-MAR-2003.  
PA (NIJJ/) NI J.  
PA (YOUN/) YOUNG P E.  
PA (KENN/) KENNY J J.  
PA (OLSE/) OLSEN H S.  
PA (MOOR/) MOORE P A.  
PA (WEIY/) WEI Y.  
PA (GREE/) GREENE J M.  
PA (RUBE/) RUBEN S M.  
PA (LIUD/) LIU D.  
PA (CROC/) CROCKER P R.  
Query Match 12.2%; Score 220.5; DB 6; Length 364;  
Best Local Similarity 26.0%; Pred. No. 2.7e-10;  
RESULT 1366  
ID AD86588 standard; protein; 364 AA.  
DE Novel human secreted protein #11.  
PN US2003129685-A1.  
PD 10-JUL-2003.  
PA (NIJJ/) NI J.  
PA (YOUN/) YOUNG P E.  
PA (KENN/) KENNY J J.  
PA (OLSE/) OLSEN H S.  
PA (MOOR/) MOORE P A.  
PA (WEIY/) WEI Y.  
PA (GREE/) GREENE J M.  
PA (RUBE/) RUBEN S M.  
Query Match 12.2%; Score 220.5; DB 8; Length 364;  
Best Local Similarity 26.0%; Pred. No. 2.7e-10;  
RESULT 1367  
ID ADR41469 standard; protein; 370 AA.  
DE Human CD-like molecule HATCZ07, SEQ ID NO:268.  
PN WO200226930-A2.  
PD 04-APR-2002.  
PA (HOMA-) HUMAN GENOME SCI INC.  
Query Match 12.2%; Score 220.5; DB 5; Length 370;  
Best Local Similarity 26.0%; Pred. No. 2.7e-10;  
RESULT 1368  
ID AAM23691 standard; protein; 402 AA.  
DE Human EST encoded protein SEQ ID NO: 1216.  
PN WO200154477-A2.  
PD 02-AUG-2001.  
PA (HYSE-) HYSEQ INC.  
Query Match 12.2%; Score 220.5; DB 4; Length 402;  
Best Local Similarity 26.0%; Pred. No. 3.1e-10;  
RESULT 1369  
ID AAY45093 standard; protein; 423 AA.  
DE Mouse lymphoid derived dendritic cell adhesion molecule.  
PN WO200008158-A2.  
PD 17-FEB-2000.  
PA (IMMV) IMMUNEX CORP.  
Query Match 12.2%; Score 220.5; DB 3; Length 423;  
Best Local Similarity 26.0%; Pred. No. 3.3e-10;  
RESULT 1370  
ID ABO84564 standard; protein; 425 AA.  
DE Human cancer-associated protein HP16-039.1.  
PN WO2004074320-A2.  
PD 02-SEP-2004.  
PA (SAGR-) SAGRES DISCOVERY INC.  
Query Match 12.2%; Score 220.5; DB 8; Length 425;  
Best Local Similarity 26.0%; Pred. No. 3.3e-10;  
RESULT 1371  
ID AAY17830 standard; protein; 440 AA.  
DE Human PRO355 protein sequence.  
PN WO9928462-A2.  
PD 10-JUN-1999.  
PA (GETH) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 2; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1372  
ID AAB01321 standard; protein; 440 AA.  
DE Human PRO355 polypeptide.  
PN WO200032776-A2.  
PD 08-JUN-2000.  
PA (GETH) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 3; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1373  
ID AAU29040 standard; protein; 440 AA.  
DE Human PRO polypeptide sequence #17.  
PN WO200168848-A2.  
PD 20-SEP-2001.  
PA (GETH) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 4; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1374  
ID ABU59416 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003027272-A1.  
PD 06-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1375  
ID ABU87964 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003032127-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1376  
ID ASU84279 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003032112-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1377  
ID ABR66153 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003027278-A1.  
PD 06-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1378  
ID ABR65543 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003036159-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1379  
ID ABU99483 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003040070-A1.  
PD 27-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1380  
ID ABU55930 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO355.  
PN US2002142959-A1.  
PD 03-OCT-2002.  
PA (GETH) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1381  
ID ASU82722 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003032113-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1382  
ID ABU89943 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003036147-A1.  
PD 20-FEB-2003.



Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1383  
ID ABR68092 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003027264-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1384  
ID ABU96145 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003036144-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1385  
ID ABU92576 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003036149-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1386  
ID AB008653 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003044923-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1387  
ID AB002705 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003040062-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1388  
ID ABR74859 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003040056-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1389  
ID ABR94621 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003044926-A1.  
PD 06-MAR-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1390  
ID ABU60240 standard; protein; 440 AA.  
DE Human PRO polypeptide #11.  
PN US2002132768-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1391  
ID ABU85594 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003036140-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1392  
ID ABU98754 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003013153-A1.  
PD 16-JAN-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;

Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1393  
ID ABU97969 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003017544-A1.  
PD 23-JAN-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1394  
ID ABU91675 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003027277-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1395  
ID ABU89368 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003036141-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1396  
ID ABU86209 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003036146-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1397  
ID ABU67422 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003036162-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1398  
ID ABU80450 standard; protein; 440 AA.  
DE Human PRO protein #17.  
PN US2003036137-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1399  
ID ABR99368 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003040063-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1400  
ID ABR98758 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003040064-A1.  
PD 27-FEB-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1401  
ID ABO16281 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003027267-A1.  
PD 06-FEB-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;  
RESULT 1402  
ID ABR92181 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003036160-A1.  
PD 20-FEB-2003.  
Query Match  
Best Local Similarity 12.2%; Score 220.5; DB 6; Length 440;

Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1403  
ID ABO18822 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003044925-A1.  
PD 06-MAR-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1404  
ID ABR78243 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003054474-A1.  
PD 20-MAR-2003.  
PA (GETH) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1405  
ID ABU64926 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein PRO355.  
PN US2002173463-A1.  
PD 21-NOV-2002.  
PA (GETH) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1406  
ID ABU84979 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003032114-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1407  
ID ABO00118 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003032101-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1408  
ID ABO11450 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003036124-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1409  
ID ABO02095 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003040054-A1.  
PD 27-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1410  
ID ABU58360 standard; protein; 440 AA.  
DE Novel human secreted protein PRO355.  
PN US2002150976-A1.  
PD 17-OCT-2002.  
PA (GETH) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1411  
ID ABU88669 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003036133-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1412  
ID ABU83364 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003036134-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1413  
ID ABO06165 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003022294-A1.  
PD 30-JAN-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1414  
ID ABR59201 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003027275-A1.  
PD 06-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1415  
ID ABO09263 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003027324-A1.  
PD 06-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1416  
ID ABO19127 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003036118-A1.  
PD 20-FEB-2003.  
PA (GETH) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1417  
ID ABO11145 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003036123-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1418  
ID ABR66763 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003036148-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1419  
ID ABO15976 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003040060-A1.  
PD 27-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1420  
ID ABO13682 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003044916-A1.  
PD 06-MAR-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1421  
ID ABU57246 standard; protein; 440 AA.  
DE Human PRO355 protein.  
PN US2002142958-A1.  
PD 03-OCT-2002.  
PA (GETH) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1422  
ID ABU65585 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein, SEQ ID 34.  
PN US2003036156-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;

RESULT 1423	ID ABR69312 standard; protein; 440 AA.	ID ABR69312 standard; protein; 440 AA.
DE Human PRO polypeptide #17.	DE Human secreted polypeptide PRO355, SEQ ID NO:34.	DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003032117-A1.	PN US2003036132-A1.	PN US2003036132-A1.
PD 13-FEB-2003.	PD 20-FEB-2003.	PD 20-FEB-2003.
Query Match	Query Match	Query Match
Best Local Similarity	Best Local Similarity	Best Local Similarity
12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;
RESULT 1424	RESULT 1434	RESULT 1434
ID ABO03620 standard; protein; 440 AA.	ID ABO01453 standard; protein; 440 AA.	ID ABO01453 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.	DE Human PRO polypeptide #17.	DE Human PRO polypeptide #17.
PN US2003036128-A1.	PN US2003008353-A1.	PN US2003008353-A1.
PD 20-FEB-2003.	PD 09-JAN-2003.	PD 09-JAN-2003.
Query Match	Query Match	Query Match
Best Local Similarity	Best Local Similarity	Best Local Similarity
12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;
RESULT 1425	RESULT 1435	RESULT 1435
ID ABR67068 standard; protein; 440 AA.	ID ABU81255 standard; protein; 440 AA.	ID ABU81255 standard; protein; 440 AA.
DE Human secreted polypeptide PRO355, SEQ ID NO:34.	DE Human PRO polypeptide #17.	DE Human PRO polypeptide #17.
PN US2003027266-A1.	PN US2003017542-A1.	PN US2003017542-A1.
PD 06-FEB-2003.	PD 23-JAN-2003.	PD 23-JAN-2003.
Query Match	Query Match	Query Match
Best Local Similarity	Best Local Similarity	Best Local Similarity
12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;
RESULT 1426	RESULT 1436	RESULT 1436
ID ABO15671 standard; protein; 440 AA.	ID ABR60052 standard; protein; 440 AA.	ID ABR60052 standard; protein; 440 AA.
DE Human secreted/transmembrane protein (PRO) #17.	DE Human secreted polypeptide PRO355, SEQ ID NO:34.	DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003054483-A1.	PN US2003032137-A1.	PN US2003032137-A1.
PD 20-MAR-2003.	PD 13-FEB-2003.	PD 13-FEB-2003.
Query Match	Query Match	Query Match
Best Local Similarity	Best Local Similarity	Best Local Similarity
12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;
RESULT 1427	RESULT 1437	RESULT 1437
ID ABU55952 standard; protein; 440 AA.	ID ABR67787 standard; protein; 440 AA.	ID ABR67787 standard; protein; 440 AA.
DE Human secreted/transmembrane protein, PRO355.	DE Human secreted polypeptide PRO355, SEQ ID NO:34.	DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003022298-A1.	PN US2003027269-A1.	PN US2003027269-A1.
PD 30-JAN-2003.	PD 06-FEB-2003.	PD 06-FEB-2003.
Query Match	Query Match	Query Match
Best Local Similarity	Best Local Similarity	Best Local Similarity
12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;
RESULT 1428	RESULT 1438	RESULT 1438
ID ABU65280 standard; protein; 440 AA.	ID ABR65175 standard; protein; 440 AA.	ID ABR65175 standard; protein; 440 AA.
DE Human PRO polypeptide #17.	DE Human secreted polypeptide PRO355, SEQ ID NO:34.	DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003032102-A1.	PN US2003027268-A1.	PN US2003027268-A1.
PD 13-FEB-2003.	PD 06-FEB-2003.	PD 06-FEB-2003.
Query Match	Query Match	Query Match
Best Local Similarity	Best Local Similarity	Best Local Similarity
12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;
RESULT 1429	RESULT 1439	RESULT 1439
ID ABU95225 standard; protein; 440 AA.	ID ABR68397 standard; protein; 440 AA.	ID ABR68397 standard; protein; 440 AA.
DE Novel human secreted and transmembrane protein PRO355.	DE Human secreted polypeptide PRO355, SEQ ID NO:34.	DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036117-A1.	PN US2003027274-A1.	PN US2003027274-A1.
PD 20-FEB-2003.	PD 06-FEB-2003.	PD 06-FEB-2003.
Query Match	Query Match	Query Match
Best Local Similarity	Best Local Similarity	Best Local Similarity
12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;
RESULT 1430	RESULT 1440	RESULT 1440
ID ABU71128 standard; protein; 440 AA.	ID ABR71809 standard; protein; 440 AA.	ID ABR71809 standard; protein; 440 AA.
DE Human PRO355 protein.	DE Human secreted polypeptide PRO355, SEQ ID NO:34.	DE Human secreted polypeptide PRO355, SEQ ID NO:34.
PN US2003036143-A1.	PN US2003032135-A1.	PN US2003032135-A1.
PD 20-FEB-2003.	PD 13-FEB-2003.	PD 13-FEB-2003.
Query Match	Query Match	Query Match
Best Local Similarity	Best Local Similarity	Best Local Similarity
12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;	12.2%; Score 220.5; DB 6; Length 440;
26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;	26.0%; Pred. No. 3.5e-10;
RESULT 1431	RESULT 1441	RESULT 1441
ID ABO07738 standard; protein; 440 AA.	ID ABU85289 standard; protein; 440 AA.	ID ABU85289 standard; protein; 440 AA.
DE Human PRO polypeptide #17.	DE Human PRO polypeptide #17.	DE Human PRO polypeptide #17.
PN US2003032130-A1.	PN US2003022295-A1.	PN US2003022295-A1.

DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003032105-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1444  
ID ABU94915 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003032123-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1445  
ID ABU90463 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003032108-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1446  
ID ABU83974 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003032111-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1447  
ID ABU93625 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003032119-A1.  
PD 13-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1448  
ID ABR64870 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003027263-A1.  
PD 06-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1449  
ID ABR68702 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003027271-A1.  
PD 06-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1450  
ID AB006518 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003036125-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1451  
ID ABR99063 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003040068-A1.  
PD 27-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1452  
ID ABU56311 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein, PRO355.  
PN US2002132981-A1.  
PD 19-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1453  
ID ABU56947 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.

PN US2003027280-A1.  
PD 06-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1454  
ID ABU85899 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003022300-A1.  
PD 30-JAN-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1455  
ID ABU82186 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003036136-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1456  
ID ABU87197 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003036138-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1457  
ID ABU83669 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003032109-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1458  
ID ABO08043 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003040066-A1.  
PD 27-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1459  
ID ABU60351 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2002168715-A1.  
PD 14-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1460  
ID ABU81754 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003032104-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1461  
ID ABU65918 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003036157-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1462  
ID ABR59747 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003032120-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1463  
ID ABU93935 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003036155-A1.  
PD 20-FEB-2003.

Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1464  
ID ABU99788 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003022296-A1.  
PD 30-JAN-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1465  
ID ABR6458 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003027281-A1.  
PD 06-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1466  
ID ABR90876 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003040058-A1.  
PD 27-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1467  
ID ABU94303 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003017540-A1.  
PD 23-JAN-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1468  
ID ABU79185 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003032106-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1469  
ID ABU86514 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003032129-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1470  
ID ABU86819 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003032131-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1471  
ID ABU94608 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003032103-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1472  
ID ABO04535 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003032107-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1473  
ID ABR70284 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003032139-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1474  
ID ASU98449 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003022301-A1.  
PD 30-JAN-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1475  
ID ABR65848 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003036165-A1.  
PD 20-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1476  
ID ABR64565 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003027262-A1.  
PD 06-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1477  
ID ABU79490 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003032110-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1478  
ID ASU92881 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003036142-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1479  
ID ASU95840 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003036145-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1480  
ID ABU91060 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003036154-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1481  
ID ABU90153 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003036153-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1482  
ID ABO09568 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003044931-A1.  
PD 06-MAR-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1483  
ID ABO10840 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003036150-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1484  
ID ABR70894 standard; protein; 440 AA.

DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003040069-A1.  
PD 27-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1485  
ID ABU87502 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003022293-A1.  
PD 30-JAN-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1486  
ID ABU91370 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003032128-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1487  
ID ABU84584 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003032116-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1488  
ID ABR69674 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003032122-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1489  
ID ABU80051 standard; protein; 440 AA.  
DE Human PRO protein #17.  
PN US2003036139-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1490  
ID ABU93320 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003017541-A1.  
PD 23-JAN-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1491  
ID ABO09873 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003017543-A1.  
PD 23-JAN-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1492  
ID ABO08958 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003036152-A1.  
PD 20-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1493  
ID ABU10526 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein #17.  
PN US2002127584-A1.  
PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1494  
ID ABU11312 standard; protein; 440 AA.  
DE Human pro355 protein sequence.  
PN US2002127643-A1.

PD 12-SEP-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1495  
ID ABU67131 standard; protein; 440 AA.  
DE Human PRO polypeptide #11.  
PN US2002165143-A1.  
PD 07-NOV-2002.  
PA (GETH ) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1496  
ID ABU95535 standard; protein; 440 AA.  
DE Human PRO polypeptide #17.  
PN US2003032115-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1497  
ID ABU6744 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003032140-A1.  
PD 13-FEB-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1498  
ID ABR70589 standard; protein; 440 AA.  
DE Human secreted polypeptide PRO355, SEQ ID NO:34.  
PN US2003040076-A1.  
PD 27-FEB-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1499  
ID ABO04940 standard; protein; 440 AA.  
DE Novel human secreted and transmembrane protein PRO355.  
PN US2003008352-A1.  
PD 09-JAN-2003.  
PA (GETH ) GENENTECH INC.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;  
RESULT 1500  
ID ABO08348 standard; protein; 440 AA.  
DE Human secreted/transmembrane protein (PRO) #17.  
PN US2003044922-A1.  
PD 06-MAR-2003.  
Query Match 12.2%; Score 220.5; DB 6; Length 440;  
Best Local Similarity 26.0%; Pred. No. 3.5e-10;

**THIS PAGE BLANK (USPTO)**